

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 919.446 Seconds

(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-4

Perfect score: 1 gtcgcagcagcagcggtata 21

Sequence: OLIGO_NUC
Gapcp 60.0, Gapext 60.0

Scoring table: 3470272 seqs, 21671516995 residues

Searched: Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

GenEmbl: 1: gb_ba: 2: gb_hlg: 3: gb_in: 4: gb_cm: 5: gb_cv: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vi: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pac: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vi: 30: em_hlg_hum: 31: em_hlg_inv: 32: em_hlg_other: 33: em_hlg_mus: 34: em_hlg_pln: 35: em_hlg_rtd: 36: em_hlg_mam: 37: em_hlg_vrt: 38: em_sy: 39: em_hgo_hum: 40: em_hgo_mus: 41: em_hgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	410	AF128731	AF128731 Uncultured
2	21	100.0	420	AF128692	AF128692 Uncultured
3	21	100.0	434	AF247784	AF247784 Soil clon
4	21	100.0	440	AF128656	AF128656 Uncultured
5	21	100.0	495	AF442311	AF442311 Tetrapisi
6	21	100.0	500	AF280951	AF280951 Uncultured
7	21	100.0	508	AF193254	AF193254 Uncultured
8	21	100.0	517	AF193029	AF193029 Uncultured
9	21	100.0	525	AF193103	AF193103 Uncultured
10	21	100.0	529	AF293558	AF293558 Uncultured
11	21	100.0	534	AF442312	AF442312 Tetrapisi
12	21	100.0	550	AF128705	AF128705 Uncultured
13	21	100.0	552	AF442310	AF442310 Tetrapisi
14	21	100.0	559	AF037640	AF037640 Uncultured
15	21	100.0	564	AF193243	AF193243 Uncultured
16	21	100.0	572	AF037568	AF037568 Uncultured
17	21	100.0	575	AF037566	AF037566 Uncultured
18	21	100.0	585	AF432842	AF432842 Uncultured
19	21	100.0	600	AF442309	AF442309 Tetrapisi
20	21	100.0	620	AF242747	AF242747 Uncultured
21	21	100.0	620	AF242748	AF242748 Uncultured
22	21	100.0	621	AF037626	AF037626 Uncultured
23	21	100.0	648	AF293557	AF293557 Uncultured
24	21	100.0	650	AF037620	AF037620 Uncultured
25	21	100.0	670	AF193253	AF193253 Uncultured
26	21	100.0	702	AF469392	AF469392 Uncultured
27	21	100.0	756	AF245484	AF245484 Uncultured
28	21	100.0	766	AF193246	AF193246 Uncultured
29	21	100.0	771	AF469403	AF469403 Uncultured
30	21	100.0	784	AF469398	AF469398 Uncultured
31	21	100.0	796	AF245486	AF245486 Uncultured
32	21	100.0	824	AF469407	AF469407 Uncultured
33	21	100.0	935	PFAMTSU	PFAMTSU
34	21	100.0	939	AF040972	AF040972 Hepatozoo
35	21	100.0	949	AF040974	AF040974 Plasmodiu
36	21	100.0	956	GS16SUS9	X85243 Gordonia sp
37	21	100.0	961	AF040968	AF040968 Babesia b
38	21	100.0	991	AF172925	AF172925 Uncultured
39	21	100.0	991	AF172926	AF172926 Uncultured
40	21	100.0	991	AF193166	AF193166 Uncultured
41	21	100.0	995	AF172927	AF172927 Uncultured
42	21	100.0	998	AF040976	AF040976 Eimeria m
43	21	100.0	1013	AF040975	AF040975 Eimeria m
44	21	100.0	1023	AF193167	AF193167 Uncultured
45	21	100.0	1024	AF193190	AF193190 Uncultured

ALIGNMENTS

RESULT 1
LOCUS AF128731 410 bp DNA linear BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C065 16S ribosomal RNA, partial sequence.
ACCESSION AF128731
VERSION AF128731.1 GI:4761945
KEYWORDS
SOURCE uncultured soil bacterium C065
ORGANISM uncultured soil bacterium C065
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 410)
Dunbar,J., Takala,S., Barnes,S.M., Davis,J.A. and Kuske,C.R.
Levels of bacterial community diversity in four acid soils compared
by cultivation and 16S rRNA gene cloning
Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL

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MEDLINE      99203125
REFERENCE    10103265
PUBMED      2 (bases 1 to 410)
AUTHORS     Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE       Direct Submission
JOURNAL     Submitted (15-FEB-1999) Environmental Molecular Biology, Life
            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
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            /clone="C065"
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            /product="16S ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GTGCCAGCAGCGGTAATA 21
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        171 GTGCCAGCAGCGGTAATA 191

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LOCUS      AF128692              420 bp    DNA             linear    BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium S079 16S ribosomal RNA, partial sequence.
ACCESSION  AF128692
VERSION     AF128692.1 GI:4761906
KEYWORDS
SOURCE      uncultured soil bacterium S079
ORGANISM    Bacteria; environmental samples.
REFERENCE   1 (bases 1 to 420)
            Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
            Levels of bacterial community diversity in four arid soils compared
            by cultivation and 16S rRNA gene cloning
            Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL     99203125
PUBMED      10103265
REFERENCE   2 (bases 1 to 420)
            Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
            Direct Submission
            Submitted (15-FEB-1999) Environmental Molecular Biology, Life
            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
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            /db_xref="taxon:92314"
            /clone="S079"
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            /product="16S ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GTGCCAGCAGCGGTAATA 21
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        202 GTGCCAGCAGCGGTAATA 222

RESULT 3
LOCUS      AF247784              434 bp    DNA             linear    BCT 08-SEP-2000
DEFINITION Soil clone WD5 16S ribosomal RNA gene, partial sequence.

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ACCESSION    AF247784
VERSION      AF247784.2 GI:9994208
KEYWORDS
SOURCE      soil clone WD5
ORGANISM    Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
            Sphingomonadaceae; environmental samples.
REFERENCE   1 (bases 1 to 434)
            Dejonghe,W., Goris,J., El Fantoussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
            Effect of dissemination of 2,4-dichlorophenoxyacetic acid (2,4-D)
            degradation plasmids on 2,4-D degradation and on bacterial
            community structure in two different soil horizons
            Appl. Environ. Microbiol. 66 (8), 3297-3304 (2000)
JOURNAL     20378631
MEDLINE     10919784
PUBMED      2 (bases 1 to 434)
REFERENCE   Dejonghe,W.L., Goris,J., El Fantoussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
            Direct Submission
            Submitted (23-MAR-2000) Faculty of Agricultural and Applied
            Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
            Belgium
            3 (bases 1 to 434)
            Dejonghe,W.L., Goris,J., El Fantoussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
            Direct Submission
            Submitted (08-SEP-2000) Faculty of Agricultural and Applied
            Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
            Belgium
REMARK      Sequence update by submitter
COMMENT      On Sep 8, 2000 this sequence version replaced gi:9864056.
FEATURES
SOURCE      Location/Qualifiers
            1..434
            /organism="soil clone WD5"
            /mol_type="genomic DNA"
            /db_xref="taxon:135645"
            /note="Isolated from B-horizon at a depth of 30-60 cm"
            <1..>434
            /product="16S ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GTGCCAGCAGCGGTAATA 21
        |||
        413 GTGCCAGCAGCGGTAATA 433

RESULT 4
LOCUS      AF128656              440 bp    DNA             linear    BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C0108 16S ribosomal RNA, partial
            sequence.
ACCESSION  AF128656
VERSION     AF128656
KEYWORDS    AF128656.1 GI:4761870
SOURCE      uncultured soil bacterium C0108
ORGANISM    Bacteria; environmental samples.
REFERENCE   1 (bases 1 to 440)
            Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
            Levels of bacterial community diversity in four arid soils compared
            by cultivation and 16S rRNA gene cloning
            Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL     99203125
MEDLINE     10103265
PUBMED      2 (bases 1 to 440)
REFERENCE   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
            Direct Submission
            Submitted (15-FEB-1999) Environmental Molecular Biology, Life

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Sciences Division, Los Alamos National Laboratory, M886, Los Alamos, NM 87545, USA

FEATURES
source

1. .440
/organism="uncultured soil bacterium C0108"
/mol_type="genomic DNA"
/db_xref="taxon:92278"
/clone="C0108"
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/product="16S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGTAATA 21
|||||
Db 200 GTGCCAGCAGCAGCGTAATA 220

RESULT 5
AF442311 495 bp DNA linear PLN 11-JUN-2003
LOCUS Tetrapispora arboricola small subunit ribosomal RNA gene, partial
DEFINITION sequence; mitochondrial gene for mitochondrial product.
ACCESSION AF442311 GI:31581325
VERSION AF442311.1 GI:31581325
KEYWORDS mitochondrial Tetrapispora arboricola
SOURCE Tetrapispora arboricola
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

REFERENCE 1 (bases 1 to 495)
AUTHORS Kurtzman, C.P. and Robnett, C.J.
TITLE Phylogenetic relationships among yeasts of the 'Saccharomyces complex' determined from multigene sequence analyses
JOURNAL FEMS Yeast Res. 3 (4), 417-432 (2003)
MEDLINE 22633405
PUBMED 12748053

REFERENCE 2 (bases 1 to 495)
AUTHORS Kurtzman, C.P. and Robnett, C.J.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2001) United States Department of Agriculture,
National Center for Agricultural Utilization Research, 1815 N.

University St., Peoria, IL 61604, USA
Location/Qualifiers

FEATURES
source

1. .495
/organism="Tetrapispora arboricola"
/organelle="mitochondrion"
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/strain="NRRL Y-27308"
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/clone="A314"
<1. .>495
/product="small subunit ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGTAATA 21
|||||
Db 114 GTGCCAGCAGCAGCGTAATA 134

RESULT 6
AF280951 500 bp DNA linear BCT 09-JUL-2001
LOCUS Uncultured bacterium clone Jsl1 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF280951

VERSION AF280951.1 GI:9255904
KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 500)
AUTHORS Stach, J.E., Bathe, S., Clapp, J.P. and Burns, R.G.
TITLE PCR-SSCP comparison of 16S rDNA sequence diversity in soil DNA
JOURNAL obtained using different isolation and purification methods
FEMS Microbiol. Ecol. 36 (2-3), 139-151 (2001)
PUBMED 11451518

REFERENCE 2 (bases 1 to 500)
AUTHORS Stach, J.E., Bathe, S. and Burns, R.G.
TITLE Evaluation and Optimization of DNA extraction and Purification from
JOURNAL soil by Single-Strand-Conformation Polymorphism
Unpublished

REFERENCE 3 (bases 1 to 500)
AUTHORS Stach, J.E., Bathe, S. and Burns, R.G.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2000) Biosciences, University of Kent at
Canterbury, University Rd, Canterbury, Kent CT2 7NU, England
Location/Qualifiers

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/db_xref="taxon:77133"
/clone="US11"
/note="environmental clone"
<1. .>500
/product="16S ribosomal RNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGTAATA 21
|||||
Db 135 GTGCCAGCAGCAGCGTAATA 155

RESULT 7
AY193254 508 bp DNA linear BCT 19-FEB-2003
LOCUS Uncultured bacterium clone Bol164 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY193254 GI:28436012
VERSION AY193254.1 GI:28436012

KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 508)
AUTHORS Harris, J.Kirk., Kelley, S.T. and Pace, N.R.
TITLE New perspective on uncultured bacterial phylogenetic division OP11
JOURNAL Unpublished
JOURNAL 2 (bases 1 to 508)
AUTHORS Harris, J.Kirk., Kelley, S.T. and Pace, N.R.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2002) Molecular, Cellular and Developmental
Biology, University of Colorado, Campus box 347, Boulder, CO 80309,

USA
Location/Qualifiers

1. .508
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/product="16S ribosomal RNA"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
 |||||
 430 GTGCCAGCAGCGGTAATA 450

RESULT 8

AY193029

LOCUS 517 bp DNA linear BCT 19-FRB-2003
 DEFINITION Uncultured candidate division Op11 bacterium clone WSA6 16S
 ribosomal RNA gene, partial sequence.

ACCESSION AY193029
 VERSION AY193029.1 GI:28435787
 KEYWORDS
 SOURCE uncultured candidate division Op11 bacterium

REFERENCE

1 (bases 1 to 517)
 HARRIS,J.Kirk., Kelley,S.T. and Pace,N.R.

JOURNAL New perspective on uncultured bacterial phylogenetic division Op11
 TITLE Unpublished
 AUTHORS 2 (bases 1 to 517)
 HARRIS,J.Kirk., Kelley,S.T. and Pace,N.R.

REFERENCE Direct Submission
 Submitted (10-DEC-2002) Molecular, Cellular and Developmental
 Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
 USA

FEATURES

SOURCE

Location/Qualifiers
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 /product="16S ribosomal RNA"

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 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
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 433 GTGCCAGCAGCGGTAATA 453

RESULT 9
 AY193103
 LOCUS 525 bp DNA linear BCT 19-FRB-2003
 DEFINITION Uncultured bacterium clone DA43 16S ribosomal RNA gene, partial
 sequence.

ACCESSION AY193103
 VERSION AY193103.1 GI:28435861
 KEYWORDS
 SOURCE uncultured bacterium

ORGANISM uncultured bacterium
 Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 525)
 HARRIS,J.Kirk., Kelley,S.T. and Pace,N.R.
 TITLE New perspective on uncultured bacterial phylogenetic division Op11
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 525)
 HARRIS,J.Kirk., Kelley,S.T. and Pace,N.R.

REFERENCE Direct Submission
 Submitted (10-DEC-2002) Molecular, Cellular and Developmental
 Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
 USA

FEATURES
 source
 Location/Qualifiers
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
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 431 GTGCCAGCAGCGGTAATA 451

RESULT 10

AY293558

LOCUS 529 bp DNA linear INV 05-JUN-2003
 DEFINITION Uncultured phototrophic eukaryote clone FL14G11 16S ribosomal RNA
 gene, partial sequence; chloroplast gene for chloroplast product.

ACCESSION AY293558
 VERSION AY293558.1 GI:31416275
 KEYWORDS
 SOURCE chloroplast uncultured phototrophic eukaryote

ORGANISM uncultured phototrophic eukaryote
 Eukaryota; environmental samples.

REFERENCE 1 (bases 1 to 529)
 Bonheyo,G.T., Fouke,B.W., Martin,H.G., Veysey,J., Goldenfeld,N. and
 Frias-Lopez,J.

JOURNAL Partitioning of Mineralogical, Geochemical, and Microbial Systems
 in Traverline Terraces at Yellowstone Hot Springs
 TITLE Unpublished
 AUTHORS 2 (bases 1 to 529)
 Bonheyo,G.T., Fouke,B.W., Martin,H.G., Veysey,J., Goldenfeld,N. and
 Frias-Lopez,J.

REFERENCE Direct Submission
 Submitted (08-MAY-2003) Geology, University of Illinois, 245
 Natural History Building, 1301 West Green St, Urbana, IL 61801, USA

JOURNAL Location/Qualifiers
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FEATURES
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 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
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 468 GTGCCAGCAGCGGTAATA 488

RESULT 11
 AF442312
 LOCUS 534 bp DNA linear PLN 11-JUN-2003
 DEFINITION Tetrapispora irimotensis small subunit ribosomal RNA gene,
 partial sequence; mitochondrial gene for mitochondrial product.

ACCESSION AF442312


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VERSION      AF442312.1  GI:31581326
KEYWORDS     mitochondrial Tetrapisipora iriomotensis
SOURCE       Tetrapisipora iriomotensis
ORGANISM     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
              Saccharomycetales; Saccharomycetaceae; Tetrapisipora.
REFERENCE    1 (bases 1 to 534)
AUTHORS      Kurtzman,C.P. and Robnett,C.J.
TITLE        Phylogenetic relationships among yeasts of the 'Saccharomyces
              complex' determined from multigene sequence analyses
JOURNAL      FEMS Yeast Res. 3 (4), 417-432 (2003)
MEDLINE      22633405
LOCUS        2 (bases 1 to 534)
DEFINITION   Kurtzman,C.P. and Robnett,C.J.
AUTHORS      Submitted (02-NOV-2001) United States Department of Agriculture,
              National Center for Agricultural Utilization Research, 1815 N.
              University St., Peoria, IL 61604, USA
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                /product="small subunit ribosomal RNA"

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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
154 GTGCCAGCAGCAGCGGTATA 174

RESULT 12
AF128705      550 bp  DNA  linear  BCT 10-MAY-1999
LOCUS         Uncultured soil bacterium S0212 16S ribosomal RNA, partial
DEFINITION   sequence.
ACCESSION    AF128705
VERSION      AF128705.1  GI:4761919
KEYWORDS     uncultured soil bacterium S0212
SOURCE       uncultured soil bacterium S0212
ORGANISM     Bacteria; environmental samples.
REFERENCE    1 (bases 1 to 550)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuskke,C.R.
TITLE        Levels of bacterial community diversity in four arid soils compared
              by cultivation and 16S rRNA gene cloning
JOURNAL      Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
MEDLINE      98263125
LOCUS        2 (bases 1 to 550)
DEFINITION   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuskke,C.R.
AUTHORS      Submitted (15-FEB-1999) Environmental Molecular Biology, Life
              Sciences Division, Los Alamos National Laboratory, M888, Los
              Alamos, NM 87545, USA
FEATURES     Location/Qualifiers
              1..550
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                /mol_type="genomic DNA"
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                /clone="S0212"
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                /product="16S ribosomal RNA"

ORIGIN
rRNA

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Query Match      100.0%; Score 21; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
Db          297 GTGCCAGCAGCAGCGGTATA 317

RESULT 13
AF442310      552 bp  DNA  linear  PLN 11-JUN-2003
LOCUS        Tetrapisipora nanseiensis small subunit ribosomal RNA gene,
              partial sequence; mitochondrial gene for mitochondrial product.
DEFINITION   AF442310
AUTHORS      Kurtzman,C.P. and Robnett,C.J.
TITLE        Phylogenetic relationships among yeasts of the 'Saccharomyces
              complex' determined from multigene sequence analyses
JOURNAL      FEMS Yeast Res. 3 (4), 417-432 (2003)
MEDLINE      22633405
LOCUS        2 (bases 1 to 552)
DEFINITION   Kurtzman,C.P. and Robnett,C.J.
AUTHORS      Submitted (02-NOV-2001) United States Department of Agriculture,
              National Center for Agricultural Utilization Research, 1815 N.
              University St., Peoria, IL 61604, USA
FEATURES     Location/Qualifiers
              1..552
                /organism="Tetrapisipora nanseiensis"
                /organella="mitochondrion"
                /mol_type="genomic DNA"
                /strain="NRRL Y-27310"
                /db_xref="taxon:113607"
                /clone="A316"
                <1..>552
                /product="small subunit ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 21; DB 8; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
Db          177 GTGCCAGCAGCAGCGGTATA 197

RESULT 14
AY037640      559 bp  DNA  linear  BCT 05-MAR-2002
LOCUS        Uncultured soil bacterium clone S133 16S ribosomal RNA gene,
              partial sequence.
DEFINITION   AY037640
ACCESSION    AY037640
VERSION      AY037640.1  GI:15789072
KEYWORDS     uncultured soil bacterium
SOURCE       uncultured soil bacterium
ORGANISM     Bacteria; environmental samples.
REFERENCE    1 (bases 1 to 559)
AUTHORS      Furlong,M.A., Singleton,D.R., Coleman,D.C. and Whitman,W.B.
TITLE        Molecular and culture-based analyses of prokaryotic communities
              from an agricultural soil and the burrows and casts of the
              earthworm Lumbricus rubellus
JOURNAL      Appl. Environ. Microbiol. 68 (3), 1265-1279 (2002)

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MEDLINE 21861246
 PUBMED 11872477
 REFERENCE 2 (bases 1 to 559)
 AUTHORS Singleton,D.R., Furlong,M.A., Coleman,D.C. and Whitman,W.B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-2001) Department of Microbiology, University of Georgia, 541 Biological Sciences Bldg, Athens, GA 30602-2605, USA

FEATURES
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 1..559
 /organism="uncultured soil bacterium"
 /mol_type="genomic DNA"
 /db_xref="taxon:164851"
 /clone="S133"
 <1..>559
 /product="16S ribosomal RNA"

ORIGIN
 rRNA
 /product="16S ribosomal RNA"

Query Match 100.0%; Score 21; DB 1; Length 559;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
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 DB 411 GTGCCAGCAGCGGTAATA 431

RESULT 15
 AY193243 564 bp DNA linear BCF 19-FEB-2003
 LOCUS Uncultured bacterium clone Bol43 16S ribosomal RNA gene, partial
 DEFINITION sequence.

ACCESSION AY193243
 VERSION AY193243.1 GI:28436001

KEYWORDS
 SOURCE uncultured bacterium
 ORGANISM uncultured bacterium
 Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 564)
 AUTHORS Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
 TITLE New perspective on uncultured bacterial phylogenetic division OP11

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 564)

AUTHORS Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2002) Molecular, Cellular and Developmental Biology, University of Colorado, Campus box 347, Boulder, CO 80309, USA

FEATURES
 source
 1..564
 Location/Qualifiers

/organism="uncultured bacterium"
 /mol_type="genomic DNA"
 /isolation_source="marine sediment"
 /db_xref="taxon:77133"
 /clone="Bol43"
 /environmental_sample
 <1..>564
 /product="16S ribosomal RNA"

ORIGIN

Query Match 100.0%; Score 21; DB 1; Length 564;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTAATA 21
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 DB 444 GTGCCAGCAGCGGTAATA 464

Search completed: August 4, 2004, 07:44:21
 Job time : 921.446 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaacacagattagatacc 20

Scoring table: OLIGO_NUC
Gapop_60.0, Gapext_60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	24	3	US-09-073-465-9
2	20	100.0	195	1	US-08-227-475-7
3	20	100.0	279	4	US-09-107-532A-3170
4	20	100.0	279	4	US-09-107-532A-3171
5	20	100.0	538	3	US-08-979-586-3
6	20	100.0	538	4	US-09-577-640-3
7	20	100.0	571	3	US-09-328-111-755
8	20	100.0	619	3	US-08-953-171-2
9	20	100.0	624	3	US-09-328-111-728
10	20	100.0	660	1	US-08-114-695A-5
11	20	100.0	665	3	US-09-328-111-476
12	20	100.0	672	3	US-09-328-111-450
13	20	100.0	851	1	US-07-898-905-1
14	20	100.0	851	1	US-07-898-905-2
15	20	100.0	851	1	US-07-898-905-3
16	20	100.0	851	3	US-09-006-089-1
17	20	100.0	851	3	US-09-006-089-2
18	20	100.0	851	3	US-09-006-089-3
19	20	100.0	876	2	US-08-642-229A-4
20	20	100.0	881	5	PCT-US91-01574-13
21	20	100.0	882	2	US-07-923-871C-13
22	20	100.0	1208	2	US-09-187-946-1
23	20	100.0	1325	2	US-08-632-470-50
24	20	100.0	1336	2	US-08-437-013-3
25	20	100.0	1336	4	US-09-375-506A-3
26	20	100.0	1366	3	US-09-191-099-4
27	20	100.0	1385	4	US-09-735-567-1

28	20	100.0	1396	3	US-08-953-171-6	Sequence 6, Appli
29	20	100.0	1400	4	US-09-375-932A-5	Sequence 5, Appli
30	20	100.0	1405	3	US-09-191-099-5	Sequence 5, Appli
31	20	100.0	1407	3	US-09-193-377B-2	Sequence 2, Appli
32	20	100.0	1407	4	US-09-517-744B-1	Sequence 1, Appli
33	20	100.0	1408	2	US-08-632-470-40	Sequence 40, Appli
34	20	100.0	1413	3	US-09-191-099-1	Sequence 1, Appli
35	20	100.0	1414	3	US-09-191-099-6	Sequence 6, Appli
36	20	100.0	1415	2	US-08-632-470-52	Sequence 52, Appli
37	20	100.0	1415	3	US-09-193-377B-9	Sequence 9, Appli
38	20	100.0	1417	3	US-09-191-099-2	Sequence 2, Appli
39	20	100.0	1419	4	US-09-565-063-2	Sequence 2, Appli
40	20	100.0	1420	1	US-08-266-414-1	Sequence 1, Appli
41	20	100.0	1420	3	US-09-193-377B-4	Sequence 4, Appli
42	20	100.0	1426	3	US-09-193-377B-7	Sequence 7, Appli
43	20	100.0	1427	2	US-08-632-470-27	Sequence 27, Appli
44	20	100.0	1428	3	US-09-193-377B-1	Sequence 1, Appli
45	20	100.0	1429	3	US-09-193-377B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-073-465-9
; Sequence 9, Application US/09073465
; Patent No. 6054278
; GENERAL INFORMATION:
; APPLICANT: DODGE, Deborah E
; APPLICANT: SMITH, Doug
; TITLE OF INVENTION: RIBOSOMAL RNA GENE POLYMORPHISM BASED MICROORGANISM
; FILE REFERENCE: 4343 US
; CURRENT APPLICATION NUMBER: US/09/073.465
; CURRENT FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterial
US-09-073-465-9

Query Match 100.0%; Score 20; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGATTAGTACC 20
DB 2 GCAACAGATTAGTACC 21

RESULT 2
US-08-227-475-7/C
; Sequence 7, Application US/08227475
; Patent No. 5536674
; GENERAL INFORMATION:
; APPLICANT: Hoshina, Sadaoyori
; APPLICANT: Weinstein, I. Bernard
; TITLE OF INVENTION: DNA Oligomers For Use In Detection Of
; TITLE OF INVENTION: Microorganisms And Methods Of Using Such DNA
; TITLE OF INVENTION: Oligomers
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,691
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 34546-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-227-475-7

Query Match 100.0%; Score 20; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGTATCCC 20
Db 128 GCAACAGGATTAGTATCCC 109

RESULT 3
US-09-107-532A-3170/c
Sequence 3170, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3170:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...279
SEQUENCE DESCRIPTION: SEQ ID NO: 3170:
US-09-107-532A-3170

Query Match 100.0%; Score 20; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGTATCCC 20
Db 134 GCAACAGGATTAGTATCCC 115

RESULT 4
US-09-107-532A-3171/c
Sequence 3171, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3171:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...279
; SEQUENCE DESCRIPTION: SEQ ID NO: 3171:
US-09-107-532A-3171

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Query Match          100.0%; Score 20; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GCAACAGGATTGATACC 20
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Db       134 GCAACAGGATTGATACC 115

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RESULT 5
US-08-979-586-3

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; Sequence 3, Application US/08979586
; Patent No. 6190903
; GENERAL INFORMATION:
; APPLICANT: Weinstein, I. B., et al.
; TITLE OF INVENTION: BACTERIUM CAPABLE OF BIODEGRADATION OF WASTES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52208/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-979-586-3

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Query Match          100.0%; Score 20; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GCAACAGGATTGATACC 20
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Db       234 GCAACAGGATTGATACC 253

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RESULT 6
US-09-577-640-3
; Sequence 3, Application US/09577640
; Patent No. 6420165
; GENERAL INFORMATION:

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; APPLICANT: The Trustees of Columbia University in the City of
; TITLE OF INVENTION: Bacterium Capable of Biodegradation of Wastes
; FILE REFERENCE: 52208adpc
; CURRENT APPLICATION NUMBER: US/09/577,640
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 08/979,586
; PRIOR FILING DATE: 1997-11-26
; SOFTWARE: Patent Ver. 2.0 - beta
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 3
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Bacillus midousei
US-09-577-640-3

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Query Match          100.0%; Score 20; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GCAACAGGATTGATACC 20
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Db       234 GCAACAGGATTGATACC 253

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RESULT 7

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US-09-328-111-755
; Sequence 755, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adam
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 755
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(571)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-755

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Query Match          100.0%; Score 20; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GCAACAGGATTGATACC 20
        |||
Db       235 GCAACAGGATTGATACC 314

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RESULT 8
US-08-953-171-2
; Sequence 2, Application US/08953171
; Patent No. 6124094

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/ GENERAL INFORMATION:
/ APPLICANT: LAJOIE, CURTIS
/ APPLICANT: LAYTON, ALICE
/ APPLICANT: KELLY, CHRISTINE
/ APPLICANT: SAYLER, GARY
/ APPLICANT: STAPLETON, RAYMOND
/ TITLE OF INVENTION: ZOOGLOEAL AND HYPHOMICROBIUM
/ TITLE OF INVENTION: SEP. NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NEEDLE & ROSENBERG, P.C.
/ STREET: 127 Peachtree Street, N.E., Suite 1200
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30303-1811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/953,171
/ FILING DATE: 17-OCT-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Spratt, Gwendolyn DD
/ REGISTRATION NUMBER: 36,016
/ REFERENCE/DOCKET NUMBER: 05015.018
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404 688 0770
/ TELEFAX: 404 688 9880
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 619 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-953-171-2
/
/ Query Match
/ Best Local Similarity 100.0%; Score 20; DB 3; Length 619;
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACGATTAGATACCC 20
DB 241 GCAAAACGATTAGATACCC 260

RESULT 9
/ US-09-328-111-728/c
/ Sequence 728, Application US/09328111
/ GENERAL INFORMATION:
/ APPLICANT: Endege, Wilson O.
/ APPLICANT: Steimann, Kathleen E.
/ APPLICANT: Astie, Jon H.
/ APPLICANT: Burgess, Christopher C.
/ APPLICANT: Bushnell, Steven E.
/ APPLICANT: Carroll III, Eddie
/ APPLICANT: Carino, Theodore J.
/ APPLICANT: Dertl, Adnan
/ APPLICANT: Ford, Donna M.
/ APPLICANT: Lewis, Marcia E.
/ APPLICANT: Monahan, John E.
/ APPLICANT: Schlegel, Robert
/ TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
/ TITLE OF INVENTION: PRODUCTS
/ FILE REFERENCE: CCD-257 (US)
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/ CURRENT APPLICATION NUMBER: US/09/328,111
/ CURRENT FILING DATE: 1999-06-08
/ EARLIER APPLICATION NUMBER: US 60/088,801
/ EARLIER FILING DATE: 1998-06-10
/ NUMBER OF SEQ ID NOS: 850
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 728
/ LENGTH: 624
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) ..(624)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-09-328-111-728
/
/ Query Match
/ Best Local Similarity 100.0%; Score 20; DB 3; Length 624;
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACGATTAGATACCC 20
DB 383 GCAAAACGATTAGATACCC 364

RESULT 10
/ US-08-114-695A-5
/ Sequence 5, Application US/08114695A
/ Patent No. 5508193
/ GENERAL INFORMATION:
/ APPLICANT: Mandelbaum, Raphael T.
/ APPLICANT: Wackett, Lawrence P.
/ TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND
/ TITLE OF INVENTION: WATER
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
/ STREET: 3500 IDS CENTER
/ CITY: MINNEAPOLIS
/ STATE: MN
/ COUNTRY: USA
/ ZIP: 55402
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/114,695A
/ FILING DATE: 31-AUG-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MUEHLING, ANN M.
/ REGISTRATION NUMBER: 33,977
/ REFERENCE/DOCKET NUMBER: 600.268US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 612-339-0331
/ TELEFAX: 612-339-3061
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 660 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: rRNA
/ ORIGINAL SOURCE:
/ ORGANISM: Pseudomonas citroneilolalis
/
/ US-08-114-695A-5
/
/ Query Match
/ Best Local Similarity 85.0%; Score 20; DB 1; Length 660;
/ Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCAACAGGATTAGATACCC 20
Db 50 GCAACAGGAUAGAUACCC 69

RESULT 11

US-09-328-111-476
; Sequence 476, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 476
; LENGTH: 665
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(665)
; OTHER INFORMATION: n = A,T,C or G

US-09-328-111-476
Query Match 100.0%; Score 20; DB 3; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
Db 292 GCAACAGGATTAGATACCC 311

RESULT 12

US-09-328-111-450
; Sequence 450, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801

; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 450
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-450

Query Match 100.0%; Score 20; DB 3; Length 672;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
Db 292 GCAACAGGATTAGATACCC 311

RESULT 13

US-07-898-905-1
; Sequence 1, Application US/07898905
; Patent No. 5424187
; GENERAL INFORMATION:
; APPLICANT: Shor;Kuo
; TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
; TITLE OF INVENTION: CHLAMYDIAL GRANULOMA"
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/898,905
; FILING DATE: 19920612
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundsmo, John S.
; REGISTRATION NUMBER: 34,445
; REFERENCE/DOCKET NUMBER: UOFW-1-6521
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: Case 7

US-07-898-905-1

Query Match 100.0%; Score 20; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
Db 610 GCAACAGGATTAGATACCC 629

RESULT 14
US-07-898-905-2
; Sequence 2, Application US/07898905
; Patent No. 5424187
; GENERAL INFORMATION:
; APPLICANT: Shor;Kuo
; TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
; CHLAMYDIAL GRANULOMA"
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/898,905
; FILING DATE: 19920612
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundsmo,John,S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: UOFW-1-6521
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: Cps
US-07-898-905-2

Query Match 100.0%; Score 20; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAACAGGATTAGATACCC 20
Db 610 GCAACAGGATTAGATACCC 629

RESULT 15
US-07-898-905-3
; Sequence 3, Application US/07898905
; Patent No. 5424187
; GENERAL INFORMATION:
; APPLICANT: Shor;Kuo
; TITLE OF INVENTION: "DIAGNOSIS AND TREATMENT OF ARTERIAL
; CHLAMYDIAL GRANULOMA"
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage

COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/898,905
FILING DATE: 19920612
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: none
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo,John,S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: UOFW-1-6521
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: Cps
US-07-898-905-3
Query Match 100.0%; Score 20; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAACAGGATTAGATACCC 20
Db 610 GCAACAGGATTAGATACCC 629
Search completed: August 4, 2004, 09:23:22
Job time : 37.1446 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 39.759 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: us-09-940-860-3

Perfect score: 22

Sequence: 1 acaagcccgagacgtattca 22

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/2/ina/5B-COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/5A-COMB.seq:*
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- 5: /cgn2_6/prodata/2/ina/PTUS-COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	100.0	368	2	US-07-923-871C-36
C 2	22	100.0	370	2	US-07-923-871C-35
C 3	22	100.0	498	2	US-07-923-871C-1
C 4	22	100.0	505	5	PCT-US91-01574-1
C 5	22	100.0	1284	3	US-09-052-333A-26
C 6	22	100.0	1284	3	US-09-052-333A-27
C 7	22	100.0	1284	3	US-09-052-333A-28
C 8	22	100.0	1284	3	US-09-052-333A-29
C 9	22	100.0	1284	3	US-09-052-333A-31
C 10	22	100.0	1408	2	US-08-632-470-40
C 11	22	100.0	1427	2	US-08-632-470-27
C 12	22	100.0	1432	2	US-08-632-470-25
C 13	22	100.0	1432	2	US-08-632-470-32
C 14	22	100.0	1436	2	US-08-632-470-34
C 15	22	100.0	1438	2	US-08-632-470-24
C 16	22	100.0	1439	2	US-08-632-470-31
C 17	22	100.0	1439	2	US-08-632-470-42
C 18	22	100.0	1440	2	US-08-632-470-23
C 19	22	100.0	1440	2	US-08-632-470-26
C 20	22	100.0	1440	2	US-08-632-470-28
C 21	22	100.0	1440	2	US-08-632-470-29
C 22	22	100.0	1440	2	US-08-632-470-33
C 23	22	100.0	1440	2	US-08-632-470-35
C 24	22	100.0	1440	2	US-08-632-470-36
C 25	22	100.0	1440	2	US-08-632-470-37
C 26	22	100.0	1440	2	US-08-632-470-39
C 27	22	100.0	1440	2	US-08-632-470-41

C 28	22	100.0	1440	2	US-08-632-470-43	Sequence 43, Appl
C 29	22	100.0	1440	2	US-08-632-470-46	Sequence 46, Appl
C 30	22	100.0	1441	2	US-08-632-470-38	Sequence 38, Appl
C 31	22	100.0	1442	2	US-08-632-470-30	Sequence 30, Appl
C 32	22	100.0	1458	2	US-08-632-470-45	Sequence 45, Appl
C 33	22	100.0	1484	2	US-08-632-470-53	Sequence 53, Appl
C 34	22	100.0	1508	2	US-08-632-470-44	Sequence 44, Appl
C 35	22	100.0	1230025	4	US-09-198-452A-1	Sequence 1, Appl
C 36	16	72.7	683	1	US-08-147-891-1	Sequence 1, Appl
C 37	16	72.7	683	1	US-08-943-464-1	Sequence 1, Appl
C 38	16	72.7	683	1	US-08-943-464-2	Sequence 2, Appl
C 39	16	72.7	683	4	US-09-491-384-1	Sequence 1, Appl
C 40	16	72.7	683	4	US-09-491-384-2	Sequence 2, Appl
C 41	16	72.7	683	4	US-09-061-770-1	Sequence 1, Appl
C 42	16	72.7	683	4	US-09-061-770-2	Sequence 2, Appl
C 43	16	72.7	938	2	US-08-879-128-1	Sequence 1, Appl
C 44	16	72.7	1435	2	US-08-632-470-48	Sequence 48, Appl
C 45	16	72.7	1494	2	US-08-632-470-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-07-923-871C-36/c
; Sequence 36, Application US/07923871C
; Patent No. 5912117
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,871C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-923-871C-36

Query Match 100.0%; Score 22; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGCCCGAGACGTATTCA 22

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Db      273 ACAAGGCCGAGAACGTATTCA 252
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RESULT 2
US-07-923-871C-35/c
; Sequence 35, Application US/07923871C
; Patent No. 5912117
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/923,871C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (35..36)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (67)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (164..165)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (167)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (169)
; US-07-923-871C-1

Query Match      100.0%; Score 22; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ACAAGGCCGAGAACGTATTCA 22
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Db      275 ACAAGGCCGAGAACGTATTCA 254
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Query Match      100.0%; Score 22; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ACAAGGCCGAGAACGTATTCA 22
|||||
Db      275 ACAAGGCCGAGAACGTATTCA 254
|||||

RESULT 3
US-07-923-871C-1/c
; Sequence 1, Application US/07923871C
; Patent No. 5912117
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA

RESULT 4
PCT-US91-01574-1/c
; Sequence 1, Application PC/TUS9101574
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA

Query Match      100.0%; Score 22; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ACAAGGCCGAGAACGTATTCA 22
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Db      396 ACAAGGCCGAGAACGTATTCA 375
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ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01574
FILING DATE: 19910307
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.
REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 2536.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3444
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: unsure
LOCATION: complement (35...36)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (41)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (67)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (164...165)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (167)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (169)
PCT-US91-01574-1

Query Match 100.0%; Score 22; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22
Db 396 ACAAGGCCCGAGACGTATTCA 375

RESULT 5
US-09-052-333A-26/c
Sequence 26, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street

CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052.333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: CWL-029
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 222..444
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 1..537
OTHER INFORMATION: /note= "Region A - Region of the
Intergenic Spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 959..1086
OTHER INFORMATION: /note= "Region B - The 3' End of
Domain I in the 23S rRNA"
US-09-052-333A-26

Query Match 100.0%; Score 22; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22
Db 67 ACAAGGCCCGAGACGTATTCA 46

RESULT 6
US-09-052-333A-27/c
Sequence 27, Application US/09052333A
Patent No. 6261769

GENERAL INFORMATION:
 APPLICANT: Everett, Karin D.E.
 APPLICANT: Andersen, Arthur A.
 TITLE OF INVENTION: Intergenic Spacer Target Sequence for
 Patent No. 6261769
 TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
 NUMBER OF SEQUENCES: 73
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis P. Ribando
 STREET: 1815 N. University Street
 CITY: Peoria
 STATE: IL
 COUNTRY: US
 ZIP: 61604
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/052,333A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ribando, Curtis P.
 REGISTRATION NUMBER: 27,976
 REFERENCE/DOCKET NUMBER: 0211.97
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 309/681-6513
 TELEFAX: 309/681-6688
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1284 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: rRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Chlamydia pneumoniae
 STRAIN: CWL-1011
 FEATURE:
 NAME/KEY: rRNA
 LOCATION: 1..221
 OTHER INFORMATION: /note= "16S rRNA"
 FEATURE:
 NAME/KEY: misc_RNA
 LOCATION: 222..444
 OTHER INFORMATION: /note= "intergenic spacer"
 FEATURE:
 NAME/KEY: rRNA
 LOCATION: 445..1063
 OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
 FEATURE:
 NAME/KEY: rRNA
 LOCATION: 445..1284
 OTHER INFORMATION: /note= "23S rRNA"
 FEATURE:
 NAME/KEY: misc_RNA
 LOCATION: 1..537
 OTHER INFORMATION: /note= "Region A - Region of the
 OTHER INFORMATION: Intergenic Spacer"
 FEATURE:
 NAME/KEY: rRNA
 LOCATION: 959..1086
 OTHER INFORMATION: /note= "Region B - The 3' End of
 OTHER INFORMATION: Domain I in the 23S rRNA"
 US-09-052-333A-27

Query Match 100.0%; Score 22; DB 3; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22
 Db 67 ACAAGGCCCGAGACGTATTCA 46
 RESULT 7
 US-09-052-333A-28/c
 ; Sequence 28, Application US/09052333A
 ; Patent No. 6261769
 ; GENERAL INFORMATION:
 ; APPLICANT: Everett, Karin D.E.
 ; APPLICANT: Andersen, Arthur A.
 ; TITLE OF INVENTION: Intergenic Spacer Target Sequence for
 ; Patent No. 6261769
 ; TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
 ; NUMBER OF SEQUENCES: 73
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Curtis P. Ribando
 ; STREET: 1815 N. University Street
 ; CITY: Peoria
 ; STATE: IL
 ; COUNTRY: US
 ; ZIP: 61604
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/052,333A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ribando, Curtis P.
 ; REGISTRATION NUMBER: 27,976
 ; REFERENCE/DOCKET NUMBER: 0211.97
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 309/681-6513
 ; TELEFAX: 309/681-6688
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1284 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: rRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Chlamydia pneumoniae
 ; STRAIN: FWL-12
 ; FEATURE:
 ; NAME/KEY: rRNA
 ; LOCATION: 1..221
 ; OTHER INFORMATION: /note= "16S rRNA"
 ; FEATURE:
 ; NAME/KEY: misc_RNA
 ; LOCATION: 222..444
 ; OTHER INFORMATION: /note= "intergenic spacer"
 ; FEATURE:
 ; NAME/KEY: rRNA
 ; LOCATION: 445..1063
 ; OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
 ; FEATURE:
 ; NAME/KEY: rRNA
 ; LOCATION: 445..1284
 ; OTHER INFORMATION: /note= "23S rRNA"
 ; FEATURE:
 ; NAME/KEY: misc_RNA
 ; LOCATION: 1..537
 ; OTHER INFORMATION: /note= "Region A - Region of the
 ; OTHER INFORMATION: Intergenic Spacer"

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; OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: 445..1284
; OTHER INFORMATION: /note= "23S rRNA"
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 1..537
; OTHER INFORMATION: /note= "Region A - Region of the
; OTHER INFORMATION: Intergenic Spacer"
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: 959..1086
; OTHER INFORMATION: /note= "Region B - The 3' End of
; OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-29

Query Match 100.0%; Score 22; DB 3; Length
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indel

QY 1 ACAAGGCCCGAGACGTATTC A 22
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Db 67 ACAAGGCCCGAGACGTATTC A 46

RESULT 9
US-09-052-333A-31/c
; Sequence 31, Application US/09052333A
; Patent No. 6261769
; GENERAL INFORMATION:
; APPLICANT: Everett, Karin D.E.
; APPLICANT: Andersen, Arthur A.
; TITLE OF INVENTION: Intergenic Spacer Target Sequence
; Patent No. 6261769
; TITLE OF INVENTION: Detecting and Distinguishing Chlamydia
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 N. University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: US
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,333A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P.
; REGISTRATION NUMBER: 27,976
; REFERENCE/DOCKET NUMBER: 0211.97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309/681-6513
; TELEFAX: 309/681-6688
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1284 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia pneumoniae
; STRAIN: TW-183
; FEATURE:

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NAME/KEY: rRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 222..444
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 1..537
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 959..1086
OTHER INFORMATION: /note= "Region B - The 3' End of
OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-31

Query Match 100.0%; Score 22; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGACGTATCA 22
Db 67 ACAAGGCCGAGACGTATCA 46

RESULT 10
US-08-632-470-40/c
Sequence 40, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1408 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-40

Query Match 100.0%; Score 22; DB 2; Length 1408;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGACGTATCA 22
Db 1319 ACAAGGCCGAGACGTATCA 1298

RESULT 11

US-08-632-470-27/c
Sequence 27, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1427 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-27

Query Match 100.0%; Score 22; DB 2; Length 1427;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGACGTATCA 22
Db 1322 ACAAGGCCGAGACGTATCA 1301

RESULT 12

US-08-632-470-25/c
Sequence 25, Application US/08632470
Patent No. 5976791
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE

```

;
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTTSIA RDNA OR RRNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-25
;
; Query Match 100.0%; Score 22; DB 2; Length 1432;
; Best Local Similarity 100.0%; Pred. No. 3.9e-05;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 ACAAGGCCCGAGAACGTATTCA 22
Db 1327 ACAAGGCCCGAGAACGTATTCA 1306

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; RESULT 13
; US-08-632-470-32/c
; Sequence 32, Application US/08632470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTTSIA RDNA OR RRNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-25
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; Query Match 100.0%; Score 22; DB 2; Length 1432;
; Best Local Similarity 100.0%; Pred. No. 3.9e-05;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1327 ACAAGGCCCGAGAACGTATTCA 1306

;
; RESULT 14
; US-08-632-470-34/c
; Sequence 34, Application US/08632470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTTSIA RDNA OR RRNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1436 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-34
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; Query Match 100.0%; Score 22; DB 2; Length 1436;
; Best Local Similarity 100.0%; Pred. No. 3.9e-05;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 ACAAGGCCCGAGAACGTATTCA 22
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;
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-32
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; Query Match 100.0%; Score 22; DB 2; Length 1432;
; Best Local Similarity 100.0%; Pred. No. 3.9e-05;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACAAGGCCCGAGAACGTATTCA 22
Db 1327 ACAAGGCCCGAGAACGTATTCA 1306

;
; RESULT 14
; US-08-632-470-34/c
; Sequence 34, Application US/08632470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTTSIA RDNA OR RRNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1436 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-34
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; Query Match 100.0%; Score 22; DB 2; Length 1436;
; Best Local Similarity 100.0%; Pred. No. 3.9e-05;
; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACAAGGCCCGAGAACGTATTCA 22
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Db 1331 ACAAGGCCCGAGACGTATTCA 1310

RESULT 15
 US-08-632-470-24/C
 ; Sequence 24, Application US/08632470
 ; Patent No. 5976791
 ; GENERAL INFORMATION:
 ; APPLICANT: NABILAT, CLAUDE
 ; APPLICANT: RAOULT, DIDIER
 ; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
 ; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
 ; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OLIFF & BERRIDGE
 ; STREET: P.O. BOX 19928
 ; CITY: ALEXANDRIA
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/632,470
 ; FILING DATE: 08-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BERRIDGE, WILLIAM P
 ; REGISTRATION NUMBER: 30,024
 ; REFERENCE/DOCKET NUMBER: WPB 38238
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)-836-6400
 ; TELEFAX: (703)-836-2787
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1438 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-632-470-24

Query Match 100.0%; Score 22; DB 2; Length 1438;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGACGTATTCA 22
 Db 1333 ACAAGGCCCGAGACGTATTCA 1312

Search completed: August 4, 2004, 09:23:29
 Job time : 40.759 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaagcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	1548	US-09-726-774-11	Sequence 11, Appl
2	20	100.0	2751	US-09-052-333A-6	Sequence 6, Appl
3	20	100.0	2762	US-09-052-333A-37	Sequence 37, Appl
4	20	100.0	1230025	US-09-198-452A-1	Sequence 1, Appl
5	16	80.0	420	US-09-252-991A-11029	Sequence 11029, A
6	16	80.0	1107	US-09-252-991A-13336	Sequence 13336, A
7	16	80.0	1179	US-09-252-991A-13193	Sequence 13193, A
8	16	80.0	1308	US-09-252-991A-12614	Sequence 12614, A
9	16	80.0	1683	US-09-252-991A-11226	Sequence 11226, A
10	16	80.0	1974	US-09-252-991A-11111	Sequence 11111, A
11	16	80.0	2283	US-09-252-991A-10956	Sequence 10956, A
12	15	75.0	191	US-09-621-976-8573	Sequence 8573, Ap
13	15	75.0	752	US-08-818-1112-2	Sequence 2, Appl
14	15	75.0	752	US-08-818-111-2	Sequence 2, Appl
15	15	75.0	752	US-09-056-556-2	Sequence 2, Appl
16	15	75.0	752	US-09-072-596-2	Sequence 2, Appl
17	15	75.0	752	US-09-072-967-2	Sequence 2, Appl
18	15	75.0	889	US-09-050-739-5	Sequence 5, Appl
19	15	75.0	1245	US-09-252-991A-6286	Sequence 6286, Ap
20	15	75.0	1980	US-09-252-991A-6369	Sequence 6369, Ap
21	15	75.0	2499	US-09-252-991A-6182	Sequence 6182, Ap
22	15	75.0	4403765	US-09-103-840A-2	Sequence 2, Appl
23	15	75.0	4411529	US-09-103-840A-1	Sequence 1, Appl
24	14	70.0	396	US-09-252-991A-6707	Sequence 6707, Ap
25	14	70.0	541	US-09-743-207-13	Sequence 13, Appl
26	14	70.0	738	US-09-252-991A-2237	Sequence 2237, Ap
27	14	70.0	895	US-09-252-991A-10382	Sequence 10382, A

C 28 14 70.0 1206 4 US-09-489-039A-4798 Sequence 4798, Ap
C 29 14 70.0 1260 4 US-09-252-991A-6674 Sequence 6674, Ap
C 30 14 70.0 1717 4 US-09-673-395A-11 Sequence 11, Appl
C 31 14 70.0 1734 4 US-09-252-991A-2607 Sequence 2607, Ap
C 32 14 70.0 2016 4 US-09-252-991A-2445 Sequence 2445, Ap
C 33 14 70.0 2141 4 US-09-620-312D-635 Sequence 635, App
C 34 14 70.0 2163 4 US-09-252-991A-6641 Sequence 6641, Ap
C 35 14 70.0 2169 4 US-09-252-991A-10268 Sequence 10268, A
C 36 14 70.0 2637 4 US-09-735-934A-1 Sequence 1, Appl
C 37 14 70.0 2637 4 US-10-060-332-1 Sequence 3, Appl
C 38 14 70.0 3437 3 US-08-450-962-3 Sequence 3, Appl
C 39 14 70.0 3437 4 US-08-848-631-3 Sequence 1, Appl
C 40 14 70.0 8906 2 US-08-836-267-1 Sequence 3, Appl
C 41 14 70.0 17138 3 US-09-813-819-3 Sequence 3, Appl
C 42 14 70.0 17138 4 US-09-920-048-3 Sequence 3, Appl
C 43 14 70.0 43950 4 US-09-735-934A-3 Sequence 3, Appl
C 44 14 70.0 43950 4 US-10-060-332-3 Sequence 3, Appl
C 45 13 65.0 20 4 US-09-302-681-91 Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-726-774-11
; Sequence 11, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-726-774-11

Query Match 100.0%; Score 20; DB 4; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGAGGAGCGGAGGATGACG 20
Db 1179 CGAGGAGCGGAGGATGACG 1198

RESULT 2
US-09-052-333A-6
; Sequence 6, Application US/09052333A
; Patent No. 6261769
; GENERAL INFORMATION:
; APPLICANT: Everett, Karin D.F.
; APPLICANT: Andersen, Arthur A.
; TITLE OF INVENTION: Intergenic Spacer Target Sequence for
; Patent No. 6261769
; TITLE OF INVENTION: Detecting and Distinguishing Chlamydia Strains
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 N. University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: US
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ribando, Curtis P.

REGISTRATION NUMBER: 27,976

REFERENCE/DOCKET NUMBER: 0211.97

TELECOMMUNICATION INFORMATION:

TELEPHONE: 309/681-6513

TELEFAX: 309/681-6688

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2751 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: rRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Chlamydia psittaci

STRAIN: NJ1

FEATURE:

NAME/KEY: rRNA

LOCATION: 1..564

OTHER INFORMATION: /note= "16S rRNA"

FEATURE:

NAME/KEY: misc RNA

LOCATION: 565..788

OTHER INFORMATION: /note= "intergenic spacer"

FEATURE:

NAME/KEY: rRNA

LOCATION: 789..1409

OTHER INFORMATION: /note= "Domain I of the 23S rRNA"

FEATURE:

NAME/KEY: rRNA

LOCATION: 789..2751

OTHER INFORMATION: /note= "23S rRNA"

FEATURE:

NAME/KEY: misc RNA

LOCATION: 345..881

OTHER INFORMATION: /note= "Region A - Region of the

INTERGENIC SPACER"

FEATURE:

NAME/KEY: rRNA

LOCATION: 1303..1432

OTHER INFORMATION: /note= "Region B - The 3' End of

DOMAIN I IN THE 23S rRNA"

US-09-052-333A-6

Query Match 100.0%; Score 20; DB 3; Length 2751;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGATGACG 20

Db 193 GGAGGAAGCGGAGGATGACG 212

RESULT 3

US-09-052-333A-37

Sequence 37, Application US/09052333A

Patent No. 6261769

GENERAL INFORMATION:

APPLICANT: Everett, Karin D.E.

APPLICANT: Andersen, Arthur A.

TITLE OF INVENTION: Intergenic Spacer Target Sequence for

Patent No. 6261769

TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains

NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2762 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
STRAIN: R22
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 565..802
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 803..1424
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 803..2762
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 346..895
OTHER INFORMATION: /note= "Region A - Region of the
INTERGENIC SPACER"
FEATURE:
NAME/KEY: rRNA
LOCATION: 1320..1447
OTHER INFORMATION: /note= "Region B - The 3' End of
DOMAIN I IN THE 23S rRNA"
US-09-052-333A-37

Query Match 100.0%; Score 20; DB 3; Length 2762;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGATGACG 20

Db 193 GGAGGAAGCGGAGGATGACG 212

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RESULT 4
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (105001)..(120000)
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; NAME/KEY: misc_feature
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; LOCATION: (180001)..(195000)
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; LOCATION: (270001)..(285000)
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: (315001)..(330000)
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; NAME/KEY: misc_feature
; LOCATION: (330001)..(345000)
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; NAME/KEY: misc_feature
; LOCATION: (345001)..(360000)
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; LOCATION: (360001)..(375000)
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; NAME/KEY: misc_feature
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; LOCATION: (420001)..(435000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (435001)..(450000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (450001)..(465000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (465001)..(480000)
; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (555001)..(570000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (570001)..(585000)
; OTHER INFORMATION: n=a or c or g or t
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (615001)..(630000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (630001)..(645000)
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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (690001)..(705000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (705001)..(720000)
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NAME/KEY: misc feature
LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (735001)..(750000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (780001)..(795000)
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LOCATION: (795001)..(810000)
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NAME/KEY: misc feature
LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match 100.0%; Score 20; DB 4; Length 12300025;
Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 GGAGGAGCGGAGGATGACG 20
Db 1011866 GGAGGAGCGGAGGATGACG 1011885

RESULT 5

US-09-252-991A-11029
Sequence 11029, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11029
LENGTH: 420
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11029

Query Match 80.0%; Score 16; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 3 AGGAGCGGAGGATGA 18
Db 157 AGGAGCGGAGGATGA 172

RESULT 6

US-09-252-991A-13336/c
Sequence 13336, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13336
LENGTH: 1107
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13336

Query Match 80.0%; Score 16; DB 4; Length 1107;
Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 5 GAAGCGGAGGATGACG 20
Db 138 GAAGCGGAGGATGACG 123

RESULT 7

US-09-252-991A-13193/c
Sequence 13193, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13193
LENGTH: 1179

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13193

Query Match 80.0%; Score 16; DB 4; Length 1179;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAAGCGGAGGATGACG 20
|||||
Db 196 GAAGCGGAGGATGACG 181

RESULT 8

US-09-252-991A-12614
; Sequence 12614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12614
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12614

Query Match 80.0%; Score 16; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAAGCGGAGGATGACG 20
|||||
Db 1216 GAAGCGGAGGATGACG 1231

RESULT 9

US-09-252-991A-11226/c
; Sequence 11226, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11226
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11226

Query Match 80.0%; Score 16; DB 4; Length 1683;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGAAGCGGAGGATGA 18
|||||
Db 1089 AGGAAGCGGAGGATGA 1074

RESULT 10

US-09-252-991A-11111/c
; Sequence 11111, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11111
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11111

Query Match 80.0%; Score 16; DB 4; Length 1974;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGAAGCGGAGGATGA 18
|||||
Db 956 AGGAAGCGGAGGATGA 941

RESULT 11

US-09-252-991A-10956
; Sequence 10956, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10956
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10956

Query Match 80.0%; Score 16; DB 4; Length 2283;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGAAGCGGAGGATGA 18
|||||
Db 1856 AGGAAGCGGAGGATGA 1871

RESULT 12

US-09-621-976-8573/c
; Sequence 8573, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8573
LENGTH: 191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-8573

Query Match 75.0%; Score 15; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGA 15
Db 188 GGAGGAAGCGGAGGA 174

RESULT 13

US-08-818-112-2
Sequence 2, Application US/08818112
Patent No. 6290969

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/818,112

APPLICATION NUMBER: US/08/818,112

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.411C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 752 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-818-112-2

Query Match 75.0%; Score 15; DB 3; Length 752;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGCGGAGGATGACG 20
Db 434 AAGCGGAGGATGACG 448

RESULT 14

US-08-818-111-2

Sequence 2, Application US/08818111

Patent No. 6338852

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.417C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 752 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-818-111-2

Query Match 75.0%; Score 15; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGCGGAGGATGACG 20
Db 434 AAGCGGAGGATGACG 448

RESULT 15

US-09-056-556-2

Sequence 2, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

TREATM

```

: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/056,556
: FILING DATE: 07-APR-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Maki, David J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/DOCKET NUMBER: 210121.457
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 752 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-09-056-556-2

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Query Match 75.0%; Score 15; DB 4; Length 752;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 AAGCGGAGGATGACG 20
Db 434 AAGCGGAGGATGACG 448

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 190.012 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-4

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Sequence: 1 GTGCCAGCAGCGCGTAATA 21

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	11 US-09-940-860-4	Sequence 4, Appli
C 2	17	81.0	1980	17 US-10-437-963-78545	Sequence 78545, A
C 3	17	81.0	3502	16 US-10-369-493-27667	Sequence 27667, A
4	16	76.2	407	10 US-09-535-459-1484	Sequence 1484, Ap
C 5	16	76.2	600	17 US-10-021-323-3179	Sequence 3179, Ap
6	16	76.2	1119	10 US-09-919-197-10	Sequence 10, Appl
C 7	16	76.2	1350	13 US-10-425-114-35039	Sequence 35039, A
C 8	16	76.2	1837	17 US-10-437-963-1280	Sequence 1280, Ap
C 9	16	76.2	1992	13 US-09-854-867-352	Sequence 352, App
C 10	16	76.2	2329	13 US-10-425-114-1420	Sequence 1420, Ap
C 11	16	76.2	3672	13 US-10-282-122A-31366	Sequence 31366, A
C 12	15	71.4	280	10 US-09-535-459-1477	Sequence 1477, Ap
C 13	15	71.4	296	10 US-09-535-459-1478	Sequence 1478, Ap
C 14	15	71.4	364	10 US-09-535-459-1475	Sequence 1475, Ap

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c 15 15 71.4 391 10 US-09-535-459-1479 Sequence 1479, Ap
16 15 71.4 483 17 US-10-437-963-41773 Sequence 41773, A
17 15 71.4 493 13 US-10-027-632-137746 Sequence 137746,
18 15 71.4 493 13 US-10-027-632-137747 Sequence 137747,
19 15 71.4 493 13 US-10-027-632-137748 Sequence 137748,
20 15 71.4 493 16 US-10-027-632-137746 Sequence 137746,
21 15 71.4 493 16 US-10-027-632-137747 Sequence 137747,
22 15 71.4 493 16 US-10-027-632-137748 Sequence 137748,
23 15 71.4 554 10 US-09-535-459-1481 Sequence 1481, Ap
c 24 15 71.4 562 13 US-10-424-599-124900 Sequence 124900,
c 25 15 71.4 590 17 US-10-021-323-3413 Sequence 3413, Ap
26 15 71.4 650 13 US-10-027-632-215667 Sequence 215667,
27 15 71.4 650 13 US-10-027-632-215668 Sequence 215668,
28 15 71.4 650 16 US-10-027-632-215667 Sequence 215667,
29 15 71.4 650 16 US-10-027-632-215668 Sequence 215668,
c 30 15 71.4 725 17 US-10-333-184-527 Sequence 527, App
c 31 15 71.4 817 17 US-10-437-963-70931 Sequence 70931, A
32 15 71.4 845 13 US-10-027-632-164886 Sequence 164886,
33 15 71.4 845 13 US-10-027-632-164887 Sequence 164887,
34 15 71.4 845 13 US-10-027-632-164888 Sequence 164888,
35 15 71.4 845 16 US-10-027-632-164886 Sequence 164886,
36 15 71.4 845 16 US-10-027-632-164887 Sequence 164887,
c 37 15 71.4 845 16 US-10-027-632-164888 Sequence 164888,
c 38 15 71.4 908 12 US-10-152-319A-2049 Sequence 2049, Ap
c 39 15 71.4 945 13 US-10-425-114-12225 Sequence 12225, A
40 15 71.4 965 13 US-10-425-114-16650 Sequence 16650, A
c 41 15 71.4 1167 13 US-10-389-647-211 Sequence 211, App
c 42 15 71.4 1173 13 US-10-282-122A-33705 Sequence 33705, A
c 43 15 71.4 1197 16 US-10-369-493-34553 Sequence 34553, A
c 44 15 71.4 1251 13 US-10-425-114-17503 Sequence 17503, A
c 45 15 71.4 1575 16 US-10-408-167A-1 Sequence 1, Appli

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ALIGNMENTS

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RESULT 1
US-09-940-860-4
; Sequence 4, Application US/09940860
; Publication No. US2004000555A1
; GENERAL INFORMATION:
; APPLICANT: Rotman, Richard
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 21
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-4

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Query Match 100.0%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTGCCAGCAGCGCGTAATA 21
Db 1 GTGCCAGCAGCGCGTAATA 21

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RESULT 2
US-10-437-963-78545/c
; Sequence 78545, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78545
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01212406
US-10-437-963-78545

Query Match 81.0%; Score 17; DB 17; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAAATA 21
Db 1018 CAGCAGCAGCGGTAAATA 1002

RESULT 3

US-10-369-493-27667/c
; Sequence 27667, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27667
; LENGTH: 3502
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27667

Query Match 81.0%; Score 17; DB 16; Length 3502;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCAGCAGCAGCGGTA 18
Db 3389 TGCAGCAGCAGCGGTA 3373

RESULT 4

US-09-535-459-1484
; Sequence 1484, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.

; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1484
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01212406
US-09-535-459-1484

Query Match 76.2%; Score 16; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCCCAGCAGCAGCGGT 17
Db 35 TCCCAGCAGCAGCGGT 50

RESULT 5

US-10-021-323-3179/c
; Sequence 3179, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 3179
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-023-Q6-K6-G3
US-10-021-323-3179

Query Match 76.2%; Score 16; DB 17; Length 600;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTA 18
Db 52 GCCAGCAGCAGCGGTA 37

RESULT 6

US-09-919-197-10
; Sequence 10, Application US/09919197
; Publication No. US20030083484A1
; GENERAL INFORMATION:
; APPLICANT: Rosaune M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: ISPH-0593
; CURRENT APPLICATION NUMBER: US/09/919,197
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(815)
US-09-919-197-10

Query Match 76.2%; Score 16; DB 10; Length 1119;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
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Db 161 GTGCCAGCAGCAGCGG 176
|||||

RESULT 7

US-10-425-114-35039/c
; Sequence 35039, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35039
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE032D03_FLI
US-10-425-114-35039

Query Match 76.2%; Score 16; DB 13; Length 1350;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCAGCAGCAGCGGTA 18
|||||
Db 170 GCCAGCAGCAGCGGTA 155
|||||

RESULT 8

US-10-437-963-1280/c
; Sequence 1280, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 1280

; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1837)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101161C.1
US-10-437-963-1280

Query Match 76.2%; Score 16; DB 17; Length 1837;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
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Db 1403 GTGCCAGCAGCAGCGG 1388
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RESULT 9

US-09-854-867-352/c
; Sequence 352, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 352
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(1992)
; OTHER INFORMATION: lipa15_5
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (760)..(760)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1149)..(1149)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)..(1261)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1418)..(1418)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1533)..(1533)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1558)..(1558)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1802)..(1802)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-352

Query Match 76.2%; Score 16; DB 13; Length 1992;
Best Local Similarity 100.0%; Pred. No. 13;


```
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1478
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01006476
US-09-535-459-1478

Query Match      71.4%; Score 15; DB 10; Length 296;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCCAGCAGCAGCGGT 17
Db      125 GCCAGCAGCAGCGGT 111

RESULT 14
US-09-535-459-1475/c
; Sequence 1475, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1475
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01109550
US-09-535-459-1475
```

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Query Match      71.4%; Score 15; DB 10; Length 364;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      3 GCCAGCAGCAGCGGT 17
Db      159 GCCAGCAGCAGCGGT 145
```

```
RESULT 15
US-09-535-459-1479/c
; Sequence 1479, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
```

```
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1479
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01224429
US-09-535-459-1479
```

```
Query Match      71.4%; Score 15; DB 10; Length 391;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GCCAGCAGCAGCGGT 17
Db      161 GCCAGCAGCAGCGGT 147
```

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Search completed: August 4, 2004, 11:56:27
Job time : 191.012 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 172.554 Seconds
(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggttaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	5849	AAV33135	Plasmodiu
2	17	81.0	1458	ABZ38180	N. gonorr
3	17	81.0	1542	AAZ12223	Neisseria
4	17	81.0	3593	ABL09563	Drosophil
5	17	81.0	6161	ABL09562	Drosophil
6	16	76.2	684	ADA31033	DNA encod
7	16	76.2	804	ADBE3858	Rat gene
8	16	76.2	804	ADD48493	Short het
9	16	76.2	1119	ABT34135	Short het
10	16	76.2	2854	ABL11243	Drosophil
11	16	76.2	3672	ACA43496	Prokaryot
12	16	76.2	5471	ABU11242	Drosophil
13	15	71.4	32	AAE60723	Murine DL
14	15	71.4	130	AAE61717	Clone VGT
15	15	71.4	197	ADD17780	DNA (Seqi
16	15	71.4	336	ABL28181	Drosophil
17	15	71.4	571	ABZ73270	Rice leaf
18	15	71.4	540	ADD16180	CDNA (Seq
19	15	71.4	716	ADD17056	DNA (Seqi
20	15	71.4	725	ABK31113	Plant dwa
21	15	71.4	908	ABT42347	Toxicity
22	15	71.4	1167	AAE81355	Quorum se
23	15	71.4	1167	ABL29451	Drosophil

C 24	15	71.4	1173	7	ACA45835	Aca45835 Prokaryot
C 25	15	71.4	1575	2	AAV02903	Aav02903 Human DNA
C 26	15	71.4	1636	3	AAA98876	Aaa98876 Human pro
C 27	15	71.4	1636	3	AAA98158	Aaa98158 Human pro
C 28	15	71.4	1636	6	AAD23987	Aad23987 Human Dha
C 29	15	71.4	1654	4	ABL117869	Ab1117869 Drosophil
C 30	15	71.4	1679	6	ABQ77568	Abq77568 Human AIP
C 31	15	71.4	1748	2	AAZ22772	Aaz22772 Human SOC
C 32	15	71.4	1748	2	AAZ22778	Aaz22778 Human SOC
C 33	15	71.4	1915	2	AAV29137	Aav29137 Homo sapi
C 34	15	71.4	2039	7	ACC44418	Acc44418 Gene enco
C 35	15	71.4	2178	7	ACA47979	Aca47979 Prokaryot
C 36	15	71.4	2186	2	AAZ20095	Aaz20095 Cytochrome
C 37	15	71.4	2196	4	AHH17305	Ahh17305 Human CDN
C 38	15	71.4	2354	9	ADB63487	Adb63487 Human CDN
C 39	15	71.4	2525	3	AAZ98625	Aaz98625 Silkworm
C 40	15	71.4	2558	2	AAZ20096	Aaz20096 Cytochrome
C 41	15	71.4	2646	4	ABL07099	Ab107099 Drosophil
C 42	15	71.4	2672	4	ABL28180	Ab128180 Drosophil
C 43	15	71.4	2860	6	ABT06279	Abt06279 Human NOV
C 44	15	71.4	2860	6	ABT06280	Abt06280 Human NOV
C 45	15	71.4	2924	9	ADD78281	Add78281 Human CGD

ALIGNMENTS

RESULT 1

AAV33135
ID AAV33135 standard; DNA; 5849 BP.
XX
AC AAV33135;
XX
DT 17-OCT-2003 (revised)
DT 07-DEC-1998 (first entry)
XX
DE Plasmodium berghei plastid PSI-PL470 gene.

XX Malaria; infection; therapy; diagnosis; vaccine; plastid; PSI-PL470 gene;
ds.

OS Plasmodium berghei; ANKA strain.

XX WO9835057-A1.

XX 13-AUG-1998.

PF 05-FEB-1998; 98WO-IB000212.

PR 06-FEB-1997; 97AU-00004953.

PR 21-APR-1997; 97AU-00006329.

XX 26-SEP-1997; 97AU-00009481.

XX (UYSI-) UNIV SINGAPORE NAT.

XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.

XX Kara AKU, Ting RCY, Tham JM, Nelson JS, Tan TMC;

XX WPI; 1998-447251/38.

XX Detecting Plasmodium infection from hybridisation with extrachromosomal
XX element - providing genus or species specific diagnosis with few false
XX negatives, in humans or animals.

XX Claim 15; Page 54-59; 120pp; English.

XX This is the nucleotide sequence of one strand of the PSI-PL470 gene of
XX the 30.7 kb extrachromosomal plastid of Plasmodium berghei. This plastid
XX encodes organelle-like RNAs, tRNAs, ribosomal proteins and RNA
XX polymerase subunits, amongst others. Plasmodium is detected in a human or
XX animal sample by treating it, or derived nucleic acid, with a Plasmodium
XX extrachromosomal genetic element or derived nucleic acid (A) and
XX detecting any hybridisation. (A) can include the PSI-PL470, PLH-PBH, PRB

CC or PWO gene, the mitochondrial cox1 gene, and nucleic acids derived from
 CC them. Also new are (A)-specific probes and primers (see AAV3139-56). The
 CC method is used to diagnose plasmodium infection. Also (not claimed) the
 CC polypeptides encoded by (A) are useful as targets for drug development
 CC and for development of anti-malaria vaccines. The high degree of
 CC similarity between (A) from different species allows development of genus
 CC - or species-specific assays that result in fewer false negatives than
 CC known methods (typically 1% against 3%). (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 5849;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGTATA 21

|||||

4671 GTGCCAGCAGCGGTATA 4691

RESULT 2

ABZ38180/C

ID ABZ38180 standard; DNA; 1458 BP.

XX

AC ABZ38180;

XX

DT 07-MAR-2003 (first entry)

XX

DE N. gonorrhoeae nucleotide sequence SEQ ID 949.

XX

KW Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX

OS Neisseria gonorrhoeae.

XX

PN WO200279243-A2.

XX

PD 10-OCT-2002.

XX

PF 12-FEB-2002; 2002WO-IB002069.

XX

PR 12-FEB-2001; 2001GB-00003424.

XX

PA (CHIR-) CHIRON SPA.

XX

PI Fontana MR, Pizza M, Maignani V, Monaci E;

XX

DR WPI; 2003-058415/05.

XX

DR P-PSDB; ABP7210.

XX

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a

XX

PS medicament for treating or preventing N. gonorrhoeae infection.

XX

PS Disclosure; Page 257; 815pp; English.

XX

CC The present invention relates to proteins from Neisseria gonorrhoeae.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
 CC molecules of the invention

XX Sequence 1458 BP; 167 A; 328 C; 569 G; 394 T; 0 U; 0 Other;

Query Match

Best Local Similarity 81.0%; Score 17; DB 7; Length 1458;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCAGCAGCAGCGGTAA 19

|||||

1067 GCCAGCAGCAGCGGTAA 1051

RESULT 3

AAZ12223/C

ID AAZ12223 standard; DNA; 1542 BP.

XX

AC AAZ12223;

XX

DT 08-OCT-1999 (first entry)

XX

DE Neisseria gonorrhoeae complete ORF139 sequence.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

XX

KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.

XX

OS Neisseria gonorrhoeae.

XX

PN WO9924578-A2.

XX

PD 20-MAY-1999.

XX

PF 09-OCT-1998; 98WO-IB001665.

XX

PR 06-NOV-1997; 97GB-00023516.

XX

PR 14-NOV-1997; 97GB-00024190.

XX

PR 18-NOV-1997; 97GB-00024386.

XX

PR 27-NOV-1997; 97GB-00025158.

XX

PR 10-DEC-1997; 97GB-00026147.

XX

PR 14-JAN-1998; 98GB-00000759.

XX

PR 01-SEP-1998; 98GB-00019016.

XX

PA (CHIR-) CHIRON SPA.

XX

PI Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;

XX

DR WPI; 1999-327407/27.

XX

DR N-PSDB; AAZ12223.

XX

PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

XX

PT diagnosis, treatment and prevention of infection.

XX

PS Claim 9; Page 332; 524pp; English.

XX

CC Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs)

XX

CC of Neisseria meningitidis and N. gonorrhoeae which encode antigenic

XX

CC proteins (see AAV38499-Y38944). The antigenic proteins, their fragments,

XX

CC their nucleic acids and antibodies are used for diagnosis, prevention (as

XX

CC vaccines) or treatment of Neisseria infections, such as meningitis,

XX

CC septicaemia and gonorrhea. Both organisms are closely related. Fragments

XX

CC of the nucleic acids are useful as hybridisation probes and antisense

XX

CC reagents

XX

SQ Sequence 1542 BP; 175 A; 345 C; 599 G; 423 T; 0 U; 0 Other;

XX

Query Match 81.0%; Score 17; DB 2; Length 1542;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCAGCAGCAGCGGTAA 19

|||||

1148 GCCAGCAGCAGCGGTAA 1132

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23171.

KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656960/75.
XX P-PSDB; ABB65460.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 23171; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 3593 BP; 1055 A; 1047 C; 919 G; 572 T; 0 U; 0 Other;
XX
XX Query Match 81.0%; Score 17; DB 4; Length 3593;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGCACGACGACGCGTA 18
XX Db 3467 TGCACGACGACGCGTA 3483
XX
XX RESULT 5
XX ABL09562
XX ID ABL09562 standard; cDNA; 6161 BP.
XX AC ABL09562;
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 23168.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX

PA (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656960/75.
XX P-PSDB; ABB65459.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX Claim 1; SEQ ID NO 23168; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6161 BP; 1747 A; 1568 C; 1438 G; 1408 T; 0 U; 0 Other;
XX
XX Query Match 81.0%; Score 17; DB 4; Length 6161;
XX Best Local Similarity 100.0%; Pred. No. 37;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TGCACGACGACGCGTA 18
XX Db 5035 TGCACGACGACGCGTA 5051
XX
XX RESULT 6
XX ADA31033
XX ID ADA31033 standard; DNA; 684 BP.
XX AC ADA31033;
XX 20-NOV-2003 (first entry)
XX
XX DNA encoding Acinetobacter baumannii protein #2320.
XX
XX ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
XX vaccine; plant biocontrol agent.
XX
XX Acinetobacter baumannii.
XX
XX US6562958-B1.
XX 13-MAY-2003.
XX
XX 04-JUN-1999; 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton G, Bush D;
XX
XX WPI; 2003-576092/54.
XX P-PSDB; ADA35159.
XX
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, or as biocontrol agents for
XX plants.
XX
XX Example; SEQ ID NO 2320; 328pp; English.
XX
XX The invention relates to isolated Acinetobacter baumannii nucleic acids.
XX

CC The A. baumannii nucleic acids and polypeptides are useful as reagents
 CC for diagnosing a bacterial disease, as components of antibacterial
 CC vaccines, as targets for antibacterial drugs, to detect the presence of
 CC A. baumannii and other Acinetobacter species in a sample, in screening
 CC compounds for the ability to interfere with the A. baumannii life cycle
 CC or to inhibit A. baumannii infection, and as biocontrol agents for
 CC plants. The present sequence represents DNA encoding an A. baumannii
 CC protein.
 CC
 SQ Sequence 684 BP; 203 A; 127 C; 159 G; 195 T; 0 U; 0 Other;
 Query Match 76.2%; Score 16; DB 8; Length 684;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CAGCAGCAGCGGTAAT 20
 Db 170 CAGCAGCAGCGGTAAT 185
 RESULT 7
 ADEG3858/c
 ID ADE63858 standard; DNA; 804 BP.
 XX AC ADE63858;
 XX
 DT 29-JAN-2004 (first entry)
 DE Rat gene X62660, SEQ ID NO 9802.
 XX
 XX Rat; ds; gene; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 FN WO2003016475-A2.
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; X62660.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially regulated in an animal subjected to pain and a
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the
 CC specification) which is differentially expressed during pain. Note: the
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;
 Query Match 76.2%; Score 16; DB 9; Length 804;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGCCAGCAGCAGCGG 16
 Db 92 GTGCCAGCAGCAGCGG 77
 RESULT 8
 ADD48493/c
 ID ADD48493 standard; DNA; 804 BP.
 XX
 AC ADD48493;
 XX
 DT 29-JAN-2004 (first entry)
 DE Rat gene X62660, SEQ ID NO 14194.
 XX
 XX Rat; ds; gene; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 FN WO2003016475-A2.
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; X62660.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially regulated in an animal subjected to pain and a
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a

CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the
 CC specification) which encodes one of the polypeptides of the invention
 CC which is differentially expressed during pain. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;
 Query Match 76.2%; Score 16; DB 9; Length 804;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
 |||||
 Db 92 GTGCCAGCAGCAGCGG 77

RESULT 9
 ABT34135
 ID ABT34135 standard; DNA; 1119 BP.
 AC ABT34135;
 XX
 XX
 DT 12-JUN-2003 (first entry)
 DE Short heterodimer partner-1 expression mouse DNA SEQ ID NO 10.
 XX
 KW Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
 KW antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
 KW short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
 KW cardiovascular disease; infection; inflammation; tumour formation; mouse;
 KW murine; ds.
 XX
 OS Mus musculus.
 XX
 PN WO2003012033-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 17-JUL-2002; 2002WO-US023245.
 XX
 PR 31-JUL-2001; 2001US-00919197.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Crooke RM, Graham MJ;
 XX
 DR WPI; 2003-248161/24.
 DR P-PSDB; AAO27109.
 XX
 PT New antisense oligonucleotide targeted to a nucleic acid encoding short
 PT heterodimer partner-1, useful for treating diseases involving abnormal
 PT lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
 PT diseases.
 XX
 PS Example 9; Page 103-105; 121pp; English.
 XX
 CC The invention relates to a novel compound of 8 - 50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding a short heterodimer partner-

CC 1. The novel compound specifically hybridizes with a nucleic acid
 CC molecule encoding the short heterodimer partner-1, and inhibits the
 CC expression of the nucleic acid molecule. The compound, and a composition
 CC comprising it are useful for treating a disease or condition associated
 CC with the short heterodimer partner-1, particularly a condition involving
 CC abnormal lipid or cholesterol metabolism such as atherosclerosis or a
 CC cardiovascular disease. They are also useful in research and diagnostics
 CC for modulating the expression of short heterodimer partner-1. They can
 CC also be useful prophylactically in preventing or delaying infection,
 CC inflammation or tumour formation. This polynucleotide represents a mouse
 CC DNA sequence relating to the short heterodimer partner-1 of the invention

XX SQ Sequence 1119 BP; 233 A; 354 C; 289 G; 243 T; 0 U; 0 Other;
 Query Match 76.2%; Score 16; DB 7; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
 |||||
 Db 161 GTGCCAGCAGCAGCGG 176

RESULT 10
 ABL11243
 ID ABL11243 standard; cDNA; 2854 BP.
 XX ABL11243;
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28211.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB67140.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 28211; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2854 BP; 775 A; 789 C; 705 G; 595 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 4; Length 2854;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGCAGCAGCGGTAA 19
DB 2354 CCAGCAGCAGCGGTAA 2369

RESULT 11
ACA43496
ID ACA43496 standard; DNA; 3672 BP.
XX
AC ACA43496;
XX
DT 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #25153.
DE
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Pseudomonas putida.
XX
PN WO200277183-A2.
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
FF
XX
XX 21-MAR-2001; 2001US-00815242.
PR
XX 06-SEP-2001; 2001US-00948993.
PR
XX 25-OCT-2001; 2001US-0342923P.
PR
XX 08-FEB-2002; 2002US-00072851.
PR
XX 06-MAR-2002; 2002US-0362699P.
PR
XX (ELIT-) ELITRA PHARM INC.
FA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX WPI; 2003-029926/02.
DR
XX P-PSDB; ABU39626.
DR
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
PT
PS Claim 14; SEQ ID NO 31366; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway of
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC on a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3672 BP; 660 A; 1207 C; 1179 G; 626 T; 0 U; 0 Other;
Query Match 76.2%; Score 16; DB 7; Length 3672;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
DB 3545 GTGCCAGCAGCAGCGG 3560

RESULT 12
ABLI1242
ID ABLI1242 standard; cDNA; 5471 BP.
XX
AC ABLI1242;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28208.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US009231.
PF
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX P-PSDB; ABB67139.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
PT interactions.
PT
XX Claim 1; SEQ ID NO 28208; 2lpp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU01840-ABU16175) and the encoded proteins (ABU57737-
CC ABU72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5471 BP; 1481 A; 1326 C; 1238 G; 1426 T; 0 U; 0 Other;
Query Match 76.2%; Score 16; DB 4; Length 5471;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGCAGCAGCGGTAA 19
 |||||
 Db 3971 CCAGCAGCAGCGGTAA 3986

RESULT 13

AAF60723/C
 ID AAF60723 standard; DNA; 32 BP.

XX AC AAF60723;

DT 03-MAY-2001 (first entry)

XX Murine DLAD signal peptide PCR primer #1.

XX Murine; DNase; DLAD; deoxyribonuclease; endonuclease; cystic fibrosis;
 KW infectious disease; PCR primer; ss.

XX Mus musculus.

XX WO200112793-A1.

PN 22-FEB-2001.

XX 01-MAY-2000; 2000WO-JP002893.

PR 17-AUG-1999; 99JP-00230870.

XX (TANU/) TANUMA S.

XX Tanuma S, Shiohawa D;

XX WPI; 2001-218348/22.

XX Acidic deoxyribonuclease capable of divalent cation-independent cleavage
 PT of DNA under acidic even neutral pH and not inhibited by G-actin, useful
 PT in remedies for cystic fibrosis and for treatment of infectious diseases.

XX Example 3; Page 29; 61pp; Japanese.

XX The present invention relates to deoxyribonuclease (DLAD) proteins and
 CC coding sequences, (see AAF60715-6 and AAF607416-7). DLAD is an
 CC endonuclease and is capable of divalent cation-independent cleavage of
 CC DNA under acidic conditions. DLAD can be used as a substitute for DNase I
 CC in treating cystic fibrosis, and is useful in the prevention and
 CC treatment of infectious diseases. The present sequence is a PCR primer
 CC for murine DLAD signal peptide (AAF60715)

XX SQ Sequence 32 BP; 5 A; 13 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 4; Length 32;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCAGCAGCGG 16

Db 32 TGCCAGCAGCAGCGG 18

RESULT 14

AAC61717

ID AAC61717 standard; DNA; 130 BP.

XX AAC61717;

DT 15-SEP-2003 (revised)

DT 06-MAR-2001 (first entry)

XX Clone VGR18 of a gene that is differentially regulated by viral Jun.

XX Viral Jun; v-Jun; cellular Jun; c-Jun; immune system disorder;

KW haematopoietic cell disorder; autoimmune disorder; allergy; inflammation;

KW organ rejection; graft-versus-host-disease; hyperproliferative disorder;
 XX infection; food additive; storage capability; nutritional component; ss.
 XX Gallus gallus.

XX WO200061738-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009766.

XX 12-APR-1999; 99US-0128897P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Vogt PK, Fu S, Halbush BS, Bottoli ILC, Dickerson JC;

XX WPI; 2000-628402/60.

XX Isolated nucleic acid molecules from Gallus domesticus are used for
 PT diagnosis and treatment of medial conditions in mammals e.g. cancers.
 XX Claim 3; Page 92; 99pp; English.

XX The present sequence is derived from a gene that is differentially
 CC regulated by viral Jun (v-Jun) and cellular Jun (c-Jun). The
 CC polynucleotide is used to prevent, treat or ameliorate a medical
 CC condition, e.g. deficiencies or disorders of the immune system, of
 CC haematopoietic cells, autoimmune disorders, allergic conditions, organ
 CC rejection or graft-versus-host-disease, inflammation, hyperproliferative
 CC disorders, bacterial, fungal, parasitic and virus infections. It can also
 CC be used to modulate hemostatic or thrombolytic activity, regenerate
 CC tissues, increase chemotactic activity of cells, modulate mammalian
 CC metabolism, change the physical or mental state of a mammal and can be
 CC used as food additives to increase or decrease storage capabilities and
 CC nutritional components. (Updated on 15-SEP-2003 to standardise OS field)

XX SQ Sequence 130 BP; 40 A; 37 C; 30 G; 23 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 3; Length 130;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 15

Db 51 GTGCCAGCAGCAGCGG 65

RESULT 15

ADD17780/C

ID ADD17780 standard; DNA; 197 BP.

XX AC ADD17780;

XX 15-JAN-2004 (first entry)

XX DNA (SeqID 1848) that confers an altered visual phenotype in plants.
 XX ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
 KW bleaching; etching; wet leaf; stunting; elongation; texture;
 KW agronomic trait; growth regulation; dwarf variety; insect resistance;
 KW heat stress; transgenic.

XX Unidentified.

XX WO2003020741-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027880.

XX 31-AUG-2001; 2001US-0316326P.

PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
 XX
 XX WPI; 2003-300858/29.
 DR
 XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
 PT sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for
 PT conferring altered visual phenotypes in plants.
 XX
 XX Claim 1; SEQ ID NO 1848; 517pp; English.
 PS
 XX This invention relates to the identification and isolation of novel
 CC nucleic acid molecules that confer altered visual phenotypes in plants.
 CC Specifically, it refers to modifications of plant architecture and/or
 CC leaf surface features in plants, such as chlorotic, bleaching, etching,
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought
 CC will be agronomic traits beneficial to the farmer. As such, these novel
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf
 CC varieties, exhibit resistance to insects or heat stress, confer changes
 CC in pigment content such that plants have enhanced vitamin production or
 CC delayed senescence and also for example produce plants that control the
 CC production of ethylene. Furthermore, the present invention comprises
 CC generating transgenic plants, as well as reproducibly altering the visual
 CC phenotype of plant seeds, plant tissues and plant cells containing the
 CC polynucleotides described herein. This polynucleotide is a homologue of a
 CC DNA sequence that confers an altered visual phenotype when expressed in
 CC plants, the method of the invention.
 XX
 SQ Sequence 197'BP; 46 A; 66 C; 42 G; 43 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 9; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCAGCAGCAGCGGT 17
 |||||
 Db 74 GCCAGCAGCAGCGGT 60

Search completed: August 4, 2004, 06:43:39
 Job time : 174.554 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1462.92 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-4

Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estlin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_esti.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: em_gss_hum.*
 - 18: em_gss_inv.*
 - 19: em_gss_pln.*
 - 20: em_gss_vrt.*
 - 21: em_gss_fun.*
 - 22: em_gss_mam.*
 - 23: em_gss_mus.*
 - 24: em_gss_pro.*
 - 25: em_gss_rod.*
 - 26: em_gss_pbg.*
 - 27: em_gss_vrl.*
 - 28: gb_gsa1.*
 - 29: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	21	100.0	420	14	CD087130
c 2	21	100.0	1128	29	CG745724
c 3	20	95.2	315	12	BI936798
c 4	20	95.2	418	10	BE517377

c 5	18	85.7	915	28	AZ677920
c 6	17	81.0	743	14	CB832595
c 7	17	81.0	178	9	AU010207
c 8	17	81.0	252	14	CK107208
c 9	17	81.0	413	9	AU007074
c 10	17	81.0	460	12	BG632306
c 11	17	81.0	475	9	AA695154
c 12	17	81.0	524	10	AM940266
c 13	17	81.0	540	9	AI518472
c 14	17	81.0	554	10	BF331275
c 15	17	81.0	619	9	AI397756
c 16	17	81.0	643	14	CD865408
c 17	17	81.0	707	14	CD873121
c 18	17	81.0	724	12	BM584191
c 19	17	81.0	745	29	CC539904
c 20	17	81.0	750	28	AZ124708
c 21	17	81.0	774	29	CC849995
c 22	17	81.0	791	28	AQ914844
c 23	17	81.0	842	14	CK203195
c 24	17	81.0	865	14	CK203537
c 25	17	81.0	886	14	CA581282
c 26	17	81.0	933	14	CA583053
c 27	17	81.0	1101	29	CNS0025C
c 28	17	81.0	1163	13	EU598465
c 29	16	76.2	186	28	AZ269457
c 30	16	76.2	222	10	BB589921
c 31	16	76.2	225	10	BB604685
c 32	16	76.2	277	10	AW866950
c 33	16	76.2	278	13	EU648979
c 34	16	76.2	336	9	AJ281902
c 35	16	76.2	337	13	BY326251
c 36	16	76.2	337	13	BY775272
c 37	16	76.2	338	13	BY275520
c 38	16	76.2	355	12	BI138225
c 39	16	76.2	355	13	BY318904
c 40	16	76.2	359	9	AA670731
c 41	16	76.2	370	13	BY769530
c 42	16	76.2	370	29	EX218719
c 43	16	76.2	373	13	BY012711
c 44	16	76.2	374	28	BH677479
c 45	16	76.2	376	13	BY769221

ALIGNMENTS

RESULT 1
CD087130/c
LOCUS
DEFINITION
MCI-0035T-R100-D10-U.G MCI-0035 Schistosoma mansoni CDNA clone
MCI-0035T-R100-D10.G, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS
1 (bases 1 to 420)

CD087130 420 bp mRNA linear EST 14-SEP-2003
MCI-0035T-R100-D10-U.G MCI-0035 Schistosoma mansoni CDNA clone
MCI-0035T-R100-D10.G, mRNA sequence.

CD087130 GI:34638055

EST.

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

1 (bases 1 to 420)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, F.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.

Transcriptome analysis of the acelomate human parasite Schistosoma mansoni

Nat. Genet. 35 (2), 148-157 (2003)

22879926

Contact: Dr. Sergio Verjovski-Almeida

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 Brasil
 Tel.: +55-11-3091-2173
 Fax: +55-11-3091-2186
 Email: verjoe@iq.usp.br
 This sequence was derived from the FAPESP Schistosoma mansoni EST
 Genome Project. All sequences in the project were assembled and
 annotated. This entry and all the assembled sequences can be seen
 in the following URL <http://bioinfo.iq.usp.br/schisto/>
 Plate: MC1-0035T-R100 row: 10 column: D.

FEATURES

source
 1. .420
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="MC1-0035T-R100-D10.G"
 /sex="mixed pool"
 /dev_stage="cercaria"
 /lab_host="Biomphalaria glabrata"
 /clone_lib="MC1-0035"
 /note="Vector: pGEM T-easy"

ORIGIN

Query Match 100.0%; Score 21; DB 14; Length 420;
 Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

Qy 1 GTGCCAGCAGCGGTAATA 21
 |||||
 Db 31 GTGCCAGCAGCGGTAATA 11

RESULT 2

CG745724 1128 bp DNA linear GSS 24-OCT-2003
 P038-3-H12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
 genomic survey sequence.

CG745724
 CG745724.1 GI:37966650
 GSS.

ORGANISM

Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.

1. (bases 1 to 1128)
 Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
 Buntjer,J., van der Meulen,M. and Sommer,R.J.
 An integrated physical and genetic map of the nematode Pristionchus
 pacificus

Mol. Genet. Genomics 269 (5), 715-722 (2003)

JOURNAL

MEDLINE

PUBMED

12884007

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Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

Location/Qualifiers

1. .1128

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of
 the genomic DNA with EcoRI and cloning into the BAC
 vector."

ORIGIN

Query Match 100.0%; Score 21; DB 29; Length 1128;
 Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

Qy 1 GTGCCAGCAGCGGTAATA 21
 |||||
 Db 477 GTGCCAGCAGCGGTAATA 497

RESULT 3

LOCUS

DEFINITION

BI936798 316 bp mRNA linear EST 18-OCT-2001

dc89d01.x1 NICHD XGC OOI Xenopus laevis cDNA clone IMAGE:3404257 3'

similar to TR:014597 014597 NON-FUNCTIONAL FOLATE BINDING PROTEIN.

; mRNA sequence.

BI936798

BI936798.1 GI:16251270

EST.

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus.

1. (bases 1 to 316)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -400p from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .316

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clones="IMAGE:3404257"

/tissue_type="oocytes"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHD XGC OOI"

/note="Vector: pCMV-SORT6; Site 1: NotI; Site 2: SalI;

Cloned unidirectionally. Primer: Oligo dt. Average insert

size 2.2 kb. Constructed by life technologies."

ORIGIN

Query Match 95.2%; Score 20; DB 12; Length 316;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCGGTAAT 20

|||||

Db 299 GTGCCAGCAGCGGTAAT 280

RESULT 4

LOCUS

DEFINITION

BES17377 418 bp mRNA linear EST 08-AUG-2000

WHE0625_B06_C112a Wheat ABA-treated embryo cDNA library Triticum

aestivum cDNA clone WHE0625_B06_C11, mRNA sequence.

BES17377

BES17377.1 GI:9741407

EST.

Triticum aestivum (bread wheat)


```

ORGANISM      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
AUTHORS      Anderson, O.D.; Chao, S.; Han, P.S.; Hsia, C.C.; Johnson, R.R.; Kang, Y.;
              Lazo, G.R.; Miller, R.; Rausch, C.J.; Seaton, C.L.; Tong, J.C.;
              Verhey, S.D. and Walker-Simmons, M.K.
TITLE        The structure and function of the expressed portion of the wheat
              genomes - ABA-treated embryo library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Olin Anderson
              US Department of Agriculture, Agriculture Research Service, Pacific
              West Area, Western Regional Research Center
              800 Buchanan Street, Albany, CA 94710, USA
              Tel: 5105595773
              Fax: 5105595818
              Email: oanderson@ow.usda.gov
              Sequence have been trimmed to remove vector sequence and low
              quality sequence with phred score less than 20
              Seq primer: Clontech Matchmaker 3' AD primer.
              Location/Qualifiers
FEATURES
source       1..418
              /organism="Triticum aestivum"
              /mol_type="mRNA"
              /cultivar="Brevor (soft, white, winter, common wheat)"
              /db_xref="taxon:4565"
              /clone="WHE0625 B06_C11"
              /tissue_type="Seed embryo"
              /dev_stage="Mature dormant seeds"
              /lab_host="E. coli DH12S"
              /clone_lib="Wheat ABA-treated embryo cDNA library"
              /note="Vector: pGAD10; Site_1: EcoRI; Site_2: XhoI;
              Embryos were cut from mature, dormant seeds and imbibed in
              25 microM ABA (abscisic acid) in 5 mM Mes buffer, pH 5.7,
              for 12 hr at 22 C. The tissue, total RNA, and poly(A)
              RNA were prepared by Steven Verhey in M.K.
              Walker-Simmons's lab (USDA-ARS, Washington State Univ.,
              Pullman, Washington 99164-6420. A cDNA library was made
              by Clontech using a combination of random and oligo dT
              primers. Library was plated and archived by Russell
              Johnson (Colby College, ME/Walker-Simmons' lab). Plasmid
              DNA preparations and DNA sequencing were performed in the
              OD Anderson lab (all other authors)."
```

ORIGIN

```

Query Match      95.2%; Score 20; DB 10; Length 418;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1  GTCCAGCAGCAGCGCGTAAT 20
        |||||
DB      304 GTCCAGCAGCAGCGCGTAAT 285
```

RESULT 5

```

AZ677920/c      915 bp DNA linear GSS 14-DEC-2000
LOCUS           Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION      Genomic, genomic survey sequence.
```

```

ACCESSION      AZ677920
VERSION        AZ677920.1 GI:11815186
KEYWORDS       GSS.
```

```

SOURCE         Entamoeba histolytica
              Entamoeba histolytica
              Eukaryota; Entamoebidae; Entamoeba.
```

```

REFERENCE
AUTHORS        Loftus, B., Van Aken, S. and Fraser, C.
TITLE          Determination of clone end sequences from Entamoeba histolytica
              HM1:IMSS sheared DNA library
JOURNAL        Unpublished (2000)
```

```

COMMENT        Contact: Brendan J Loftus
              Department of Eukaryotic Genomics
```

```

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b1o@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 176
High quality sequence stop: 283.
```

FEATURES

```

source       1..915
              /organism="Entamoeba histolytica"
              /mol_type="genomic DNA"
              /strain="HM1:IMSS"
              /db_xref="taxon:5759"
              /clone_lib="Entamoeba histolytica Sheared DNA"
              /note="Vector: pHOSt; Site 1: Bst I; Constructed at The
              Institute for Genomic Research (TIGR), Rockville, MD.
              Genomic DNA isolated from broth cultures of E. histolytica
              using a method described by Clark and Diamond (Clark,
              C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
              method for isolate identification. Exp. Parasitol.
              77:450.). The DNA was mechanically sheared to give a
              tight size distribution (~2 kb). The v + i method used for
              the library construction is described in detail in Smith,
              H.O. and Venter, J.C. (Making small insert libraries for
              whole genome shotgun sequencing projects. In Genome
              Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999)."
```

ORIGIN

```

Query Match      85.7%; Score 18; DB 28; Length 915;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      3  GCCAGCAGCAGCGCGTAAT 20
        |||||
DB      891 GCCAGCAGCAGCGCGTAAT 874
```

RESULT 6

```

CB832595/c      73 bp mRNA linear EST 21-APR-2003
LOCUS           SWBmfcAV08B01SK Wuchereria bancrofti microfilaria cDNA
DEFINITION      (SW95Sjl-Wbmf) Wuchereria bancrofti cDNA clone SWBmfcAV08B01 5',
              mRNA sequence.
```

```

ACCESSION      CB832595
VERSION        CB832595.1 GI:30030842
KEYWORDS       EST.
```

```

SOURCE         Wuchereria bancrofti
              Wuchereria bancrofti
              Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
```

```

              Onchocercidae; Wuchereria.
              1 (bases 1 to 73)
```

```

REFERENCE
AUTHORS        Williams, S.A.
TITLE          Genes expressed in microfilaria of Wuchereria bancrofti
JOURNAL        Unpublished (1996)
COMMENT        Contact: Steven A. Williams
              Molecular Parasitology
```

```

              Smith College Department of Biological Sciences
              Department of Biological Sciences, Clark Science Center, Smith
              College, Northampton, MA, 01063, USA
              Tel: 4135853826
              Fax: 4135853786
```

```

Seq primer: pBluescript SK.
```

```

              Location/Qualifiers
FEATURES
source       1..73
```

```

              /organism="Wuchereria bancrofti"
              /mol_type="mRNA"
              /db_xref="taxon:6293"
```

/clone="SWbmfCAV08901"
 /dev stage="microfilaria"
 /lab host="XLI-Blue MRP"
 /clone lib="Wuchereria bancrofti microfilaria cDNA
 (SAW955JL-WBMF)"
 /note=vector: lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
 Xho I; Lymphatic filarial nematode parasite of humans.
 mRNA was prepared from approximately 85,000 microfilariae
 isolated from the blood of an infected individual from
 Guyana, South America and converted to double-stranded
 cDNA using reverse transcriptase and oligo(dT) followed by
 RNase H and DNA pol I. The library has 2.9 x 10E5
 independent recombinants and the average insert size is
 ~1kb. The library was constructed by Sandra J. Lane. The
 library is available from Dr.S.A.Williams, email:
 genome@smith.edu."

ORIGIN

Query Match 81.0%; Score 17; DB 14; Length 73;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAATA 21
 |||||

Db 37 CAGCAGCAGCGGTAATA 21
 |||||

RESULT 7

AU010207

LOCUS

DEFINITION AU010207 Schizosaccharomyces pombe late log phase cDNA EST 31-JUL-1998

Schizosaccharomyces pombe cDNA clone spc05561, mRNA sequence.

ACCESSION AU010207.1 GI:3346887

VERSION EST.

KEYWORDS Schizosaccharomyces pombe (fission yeast)

SOURCE Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

ORGANISM Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 148)

AUTHORS Morimyo,M. and Mita,K.

TITLE Identification of expressed sequence tags of Schizosaccharomyces

pombe

JOURNAL Unpublished (1998)

COMMENT Contact: Mitsuoki Morimyo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

Email: morimyo@nirs.go.jp.

FEATURES

source

1. .148

/organism="Schizosaccharomyces pombe"

/mol_type="RNA"

/strain="972"

/db_xref="taxon:4896"

/clone="spc05561"

/sex="h minus"

/clone lib="Schizosaccharomyces pombe late log phase cDNA"

/note=vector: M13mp19; The cDNA library of

Schizosaccharomyces pombe was prepared by cloning cDNA

into the SmaI site of M13mp19 DNA and the direction of DNA

sequences was not always from 5' to 3'. The cDNA data of

Schizosaccharomyces pombe are available for searching on

the World Wide Web. (URL, <http://www.nirs.go.jp>)"

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match

Best Local Similarity

Matches 17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy 1 GTGCCAGCAGCGGTT 17

|||||

Db 68 GTGCCAGCAGCGGTT 84

RESULT 8

CK107208

LOCUS

DEFINITION CK107208 252 bp mRNA linear EST 01-DEC-2003

UBA9DPG02.5pr Populus active cambium cDNA library Populus tremula

CDNA clone UBA9DPG02 5', mRNA sequence.

ACCESSION CK107208

VERSION CK107208.1 GI:38591533

KEYWORDS EST.

SOURCE Populus tremula

ORGANISM Populus tremula

REFERENCE 1 (bases 1 to 252)

AUTHORS Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,

Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,

Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,

Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.

A Populus EST resource for functional genomics

Unpublished (2003)

Other ESTs: UBA9DPG02, UBA9DPG02.3pr

Contact: Bo Segerman

Umea Plant Science Center, Department of Plant Physiology

Umea University

901 87 Umea, Sweden

Tel: +46 90 786 5279

Fax: +46 90 786 6676

Email: bo.segerman@plantphys.umu.se.

FEATURES

source

1. .252

/organism="Populus tremula"

/mol_type="mRNA"

/db_xref="taxon:113636"

/clone="UBA9DPG02"

/tissue type="Active cambium"

/clone lib="Populus active cambium cDNA library"

ORIGIN

Query Match

Best Local Similarity

Matches 17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy 5 CAGCAGCAGCGGTAATA 21

|||||

Db 189 CAGCAGCAGCGGTAATA 205

|||||

RESULT 9

AU007074/c

LOCUS

DEFINITION AU007074 413 bp mRNA linear EST 31-JUL-1998

Schizosaccharomyces pombe late log phase cDNA

Schizosaccharomyces pombe cDNA clone spc01418, mRNA sequence.

ACCESSION AU007074

VERSION AU007074.1 GI:3343532

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 413)

AUTHORS Morimyo,M. and Mita,K.

TITLE Identification of expressed sequence tags of Schizosaccharomyces

pombe

Unpublished (1998)

Contact: Mitsuoki Morimyo

Genome Research Group

National Institute of Radiological Sciences

9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

Email: morimyo@nirs.go.jp.

FEATURES source
 Location/Qualifiers
 1. 413
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc01418"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN
 Query Match 81.0%; Score 17; DB 9; Length 413;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
 |||||
 Db 80 GTGCCAGCAGCAGCGGT 64
 |||||

RESULT 10
 BG632306/c
 LOCUS
 DEFINITION
 melanogaster cDNA clone GH06375 3, mRNA sequence.
 ACCESSION
 BG632306
 VERSION
 BG632306.1 GI:13757423
 KEYWORDS
 EST.
 SOURCE
 Drosophila melanogaster (fruit fly)
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE
 1 (bases 1 to 460)
 AUTHORS
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
 TITLE
 BDGP/HMI Drosophila EST Project
 JOURNAL
 Unpublished (2001)
 COMMENT
 Other ESTs: GH06375.5prime
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AB003763: arm:3R (23621985,23825541)
 Estimated-cyto:98B1-98B6: 04/10/2001
 Plate: GH.63 row: G column: 3
 High quality sequence stop: 444.
 Location/Qualifiers
 1. 460
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="GH06375"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DH5 - alpha"
 /clone_lib="GH Drosophila melanogaster head pot2"
 /note="Organ: head; Vector: pot2; Site: 1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into pot2. Plasmid cDNA library."

Query Match 81.0%; Score 17; DB 12; Length 460;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCCCAGCAGCAGCGGTA 18
 |||||
 Db 156 TCCCAGCAGCAGCGGTA 140
 |||||

RESULT 11
 AA695154/c
 LOCUS
 DEFINITION
 GH02326.3prime GM Drosophila melanogaster ovary Bluescript
 Drosophila melanogaster cDNA clone GH02326 3prime, mRNA sequence.
 ACCESSION
 AA695154
 VERSION
 AA695154.1 GI:2697774
 KEYWORDS
 EST.
 SOURCE
 Drosophila melanogaster (fruit fly)
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE
 1 (bases 1 to 475)
 AUTHORS
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
 TITLE
 BDGP/HMI Drosophila EST Project
 JOURNAL
 Unpublished (2001)
 COMMENT
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
 Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone probably contains an inverted insert. The sequence has been trimmed and the T residues removed.
 Plate: 23 row: C column: 2
 High quality sequence stop: 406.
 Location/Qualifiers
 1. 475
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="GH02326"
 /sex="female"
 /dev_stage="newly eclosed females: germarium-stage 6"
 /lab_host="SOLR"
 /clone_lib="GM Drosophila melanogaster ovary Bluescript"
 /note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in Bluescript SK(+/-)"

ORIGIN
 Query Match 81.0%; Score 17; DB 9; Length 475;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCCCAGCAGCAGCGGTA 18
 |||||
 Db 156 TCCCAGCAGCAGCGGTA 140
 |||||

RESULT 12
 AA940266/c
 LOCUS
 DEFINITION
 GH07623.3prime GH Drosophila melanogaster head pot2 Drosophila melanogaster cDNA clone GH07623 3 similar to CG5514: FBan005514 GO:[] located on: 3R 98B2-98B2; 08/12/2002, mRNA sequence.
 ACCESSION
 AA940266
 VERSION
 AA940266.1 GI:8115712
 KEYWORDS
 EST.

SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 524)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Other ESTs: GH07623-5prime
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Based upon the presence of a XhoI site followed by a run of 14 or
 more T residues at the beginning of the sequence, this clone was
 polyadenylated. The resulting Poly-T sequence has been removed. hit
 genomic AE003763: Drosophila melanogaster genomic scaffold
 14200013386035 section 88 of 105, complete sequence.: 02/16/2001
 Plate: GH.76 row: B column: 11
 High quality sequence stop: 382.
 Location/Qualifiers
 1..524
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="GH07623"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DH5 - alpha"
 /clone_lib="GH Drosophila melanogaster head pOT2"
 /note="Organ: head; Vector: pOT2; Site: 1; EcoRI; Site 2:
 XhoI; Sized fractionated cDNAs were directly ligated into
 pOT2. Plasmid cDNA library."
 ORIGIN
 Query Match 81.0%; Score 17; DB 10; Length 524;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGCCAGCAGCAGCGGTA 18
 |||||
 Db 156 TGCCAGCAGCAGCGGTA 140
 RESULT 13
 A1518472/c
 LOCUS LD37996.3prime LD Drosophila melanogaster embryo pOT2 Drosophila
 DEFINITION melanogaster cDNA clone LD37996 3prime, mRNA sequence.
 ACCESSION A1518472
 VERSION A1518472.1 GI:4424326
 EST.
 SOURCE
 ORGANISM Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 540)
 Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
 Lewis, S., and Rubin, G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
 Based upon the presence of a XhoI site followed by a run of 14 or

more T residues at the beginning of the sequence, this clone
 probably contains an inverted insert. The resulting Poly-T sequence
 has been removed.
 Plate: 379 row: H column: 12
 High quality sequence stop: 440.
 Location/Qualifiers
 1..540
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="LD37996"
 /sex="male and female"
 /dev_stage="0 to 24 hours mixed stage embryonic"
 /lab_host="XLI Blue"
 /clone_lib="LD Drosophila melanogaster embryo pOT2"
 /note="Organ: embryo; Vector: pOT2; Site 1; EcoRI; Site 2:
 XhoI; Sized fractionated cDNAs were directly ligated into
 pOT2."
 ORIGIN
 Query Match 81.0%; Score 17; DB 9; Length 540;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TGCCAGCAGCAGCGGTA 18
 |||||
 Db 156 TGCCAGCAGCAGCGGTA 140
 RESULT 14
 BF331275/c
 LOCUS RCS-BT0377-030200-012-G03 BT0377 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BF331275
 VERSION BF331275.1 GI:11302023
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 554)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsumura, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Sucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 PUBLISHED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCS&st2=RCS-BT0377-030200-012-G03&t3=2000-02-03&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 74
 High quality sequence stop: 91.
 Location/Qualifiers
 1..554
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 FEATURES
 source

Db 279 GTGCCAGCAGCGGGT 263

Search completed: August 4, 2004, 09:20:58
Job time : 1466.92 secs

/clone_lib="BT0377"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCAGCAGCAGCGGTAA 19
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Db 49 GCCAGCAGCAGCGGTAA 33
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RESULT 15
AI397756/c

LOCUS
DEFINITION NCCSH8T3 Conidial Neurospora crassa cDNA clone NCSH8 5', mRNA 619 bp mRNA linear EST 08-FEB-1999

ACCESSION AI397756
VERSION AI397756.1 GI:4240841
KEYWORDS EST.

SOURCE

ORGANISM Neurospora crassa
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

REFERENCE

AUTHORS
Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,
Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E.,
Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K.,
Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S.,
Trujillo, R., Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S.
and Natvig, D.O.
Expressed sequences from conidial, mycelial, and sexual stages of
Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)

JOURNAL

MEDLINE

PUBMED

9290248

COMMENT

Contact: Natvig, D.O./Nelson, M.A.
Department of Biology
University of New Mexico
Cascetter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.

FEATURES

source

1..619
Location/Qualifiers

/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="74-OR23-IV A"
/db_xref="taxon:5141"
/clone="NCSH8"
/sex="Mating type A"
/tissue_type="Conidia"
/dev_stage="germinating conidia"
/clone_lib="Conidial"
/note="mRNA isolated from germinating conidia, grown in 1x
Vogel's, 2% sucrose for 4.5 hours. cDNA directionally
cloned into pBluescript SK(-) using the Uni-ZAP XR vector
system (Stratagene, La Jolla, CA)."

ORIGIN

Query Match 81.0%; Score 17; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCGGGT 17
|||||

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 218.94 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-3

Perfect score: 22

Sequence: 1 aacagccgcgaacgtattca 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 4: /cgn2_6/ptcdatca/2/pna/US08_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	16	72.7	1502	7 US-10-729-961-4	Sequence 4, Appli
C 2	16	72.7	1681	7 US-10-729-961-1	Sequence 1, Appli
C 3	16	72.7	8004	5 US-09-404-520B-5583	Sequence 5583, Ap
C 4	15	68.2	281443	6 US-10-896-891-531	Sequence 531, App
C 5	14	63.6	1071	7 US-10-100-683-3306	Sequence 3306, Ap
C 6	14	63.6	1080	5 US-09-404-520B-27485	Sequence 27485, A
C 7	14	63.6	1215	5 US-09-248-796A-3573	Sequence 3573, Ap
C 8	14	63.6	1271	7 US-10-767-701-12478	Sequence 12478, A
C 9	14	63.6	1378	5 US-09-404-520B-9481	Sequence 9481, Ap
C 10	14	63.6	1389	5 US-09-404-520B-20466	Sequence 20466, A
C 11	14	63.6	1553	6 US-10-425-115-166711	Sequence 166711, A
C 12	14	63.6	1866	5 US-09-404-520B-14910	Sequence 14910, A
C 13	14	63.6	1959	7 US-10-100-683-2841	Sequence 2841, Ap
C 14	14	63.6	2307	7 US-10-745-444-764	Sequence 764, App
C 15	14	63.6	2783	6 US-10-501-933-4270	Sequence 4270, Ap
C 16	14	63.6	2783	9 US-09-559-949-602	Sequence 602, App
C 17	14	63.6	10088	7 US-10-100-683-13121	Sequence 13121, A
C 18	14	63.6	67163	7 US-10-767-471-10712	Sequence 10712, A
C 19	14	63.6	77945	9 US-09-582-609-20052	Sequence 20052, A
C 20	13	59.1	19	8 US-10-714-333A-495525	Sequence 495525, A
C 21	13	59.1	19	8 US-10-714-333A-600711	Sequence 600711, A
C 22	13	59.1	25	5 US-09-860-080C-10392	Sequence 10392, A
C 23	13	59.1	25	7 US-10-843-527-118931	Sequence 118931, A
C 24	13	59.1	25	7 US-10-843-527-119246	Sequence 119246, A

C 25	13	59.1	49	5 US-09-404-520B-36908	Sequence 36908, A
C 26	13	59.1	60	9 US-60-579-902-11666	Sequence 11666, A
C 27	13	59.1	261	9 US-60-565-632-2213	Sequence 2213, Ap
C 28	13	59.1	261	9 US-60-579-082-4213	Sequence 2213, Ap
C 29	13	59.1	267	6 US-10-425-115-20380	Sequence 20380, A
C 30	13	59.1	327	7 US-10-834-967-2447	Sequence 2447, Ap
C 31	13	59.1	359	6 US-10-425-115-14666	Sequence 14666, A
C 32	13	59.1	450	5 US-09-404-520B-8744	Sequence 8744, Ap
C 33	13	59.1	450	5 US-09-404-520B-20686	Sequence 20686, A
C 34	13	59.1	471	5 US-09-404-520B-26196	Sequence 26196, A
C 35	13	59.1	480	1 PCT-US04-17686-2675	Sequence 2675, Ap
C 36	13	59.1	500	6 US-10-425-115-108619	Sequence 108619, A
C 37	13	59.1	516	7 US-10-767-701-28589	Sequence 28589, A
C 38	13	59.1	601	6 US-10-896-891-9568	Sequence 9568, Ap
C 39	13	59.1	601	6 US-10-896-891-9569	Sequence 9569, Ap
C 40	13	59.1	658	1 PCT-US04-08371A-304	Sequence 304, App
C 41	13	59.1	702	7 US-10-724-972A-2882	Sequence 2882, Ap
C 42	13	59.1	749	6 US-10-425-115-97664	Sequence 97664, A
C 43	13	59.1	750	6 US-10-425-115-164349	Sequence 164349, A
C 44	13	59.1	759	9 US-60-554-981-1436	Sequence 1436, Ap
C 45	13	59.1	1146	7 US-10-100-683-1635	Sequence 1635, Ap

ALIGNMENTS

RESULT 1

US-10-729-961-4/c

; Sequence 4, Application US/10729961

; GENERAL INFORMATION:

; APPLICANT: IWASE, Tadayuki

; APPLICANT: ITANO, Morihide

; TITLE OF INVENTION: Primers For Detecting Fusobacterium Nucleatum By Pcr Methods And

; TITLE OF INVENTION: For Detection

; FILE REFERENCE: 246312US0

; CURRENT APPLICATION NUMBER: US/10/729,961

; PRIOR FILING DATE: 2003-12-09

; PRIOR APPLICATION NUMBER: JP 2002-358698

; PRIOR FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: JP 2003-403715

; PRIOR FILING DATE: 2003-12-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1502

; TYPE: DNA

; ORGANISM: Fusobacterium nucleatum

; US-10-729-961-4

Query Match 72.7%; Score 16; DB 7; Length 1502;

Best Local Similarity 100.0%; Pred.No. 0.47; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCCGAGAACGTTATTC A 22

Db 1367 CCCGAGAACGTTATTC A 1352

RESULT 2

US-10-729-961-1/c

; Sequence 1, Application US/10729961

; GENERAL INFORMATION:

; APPLICANT: IWASE, Tadayuki

; APPLICANT: ITANO, Morihide

; TITLE OF INVENTION: Primers For Detecting Fusobacterium Nucleatum By Pcr Methods And

; TITLE OF INVENTION: For Detection

; FILE REFERENCE: 246312US0

; CURRENT APPLICATION NUMBER: US/10/729,961

; PRIOR FILING DATE: 2003-12-09

; PRIOR APPLICATION NUMBER: JP 2002-358698

; PRIOR FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: JP 2003-403715
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Fusobacterium nucleatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1650)..(1650)
; OTHER INFORMATION: n stands for any base
US-10-729-961-1

Query Match 72.7%; Score 16; DB 7; Length 1661;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
Db 1367 CCCGAGAACGTATTCA 1352

RESULT 3
US-09-404-520B-5583/c
; Sequence 5583, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 5583
; LENGTH: 8004
; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-5583

Query Match 72.7%; Score 16; DB 5; Length 8004;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
Db 771 CCCGAGAACGTATTCA 756

RESULT 4
US-10-896-891-531/c
; Sequence 531, Application US/10896891
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH CANCER, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000788
; CURRENT APPLICATION NUMBER: US/10/896,891
; CURRENT FILING DATE: 2004-07-23
; PRIOR FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 12618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 531
; LENGTH: 281443
; TYPE: DNA
; ORGANISM: Human
US-10-896-891-531

Query Match 68.2%; Score 15; DB 6; Length 281443;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GCCCGAGAACGTATT 20
Db 240133 GCCCGAGAACGTATT 240119

RESULT 5
US-10-100-683-3306
; Sequence 3306, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3306
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-3306

Query Match 63.6%; Score 14; DB 7; Length 1071;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGGCCCGAGAAC 15
Db 103 CAAGGCCCGAGAAC 116

RESULT 6
US-09-404-520B-27485
; Sequence 27485, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 27485
; LENGTH: 1080


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; TYPE: DNA
; ORGANISM: Emmericella nidulans
US-09-404-520B-27485

Query Match      63.6%; Score 14; DB 5; Length 1080;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGAGAACGTATTCA 22
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Db 904 CGAGAACGTATTCA 917

RESULT 7
US-09-248-796A-3573
; Sequence 3573, Application US/09248796A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3573
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3573

Query Match      63.6%; Score 14; DB 5; Length 1215;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAA 14
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Db 1151 ACAAGGCCCGAGAA 1164

RESULT 8
US-10-767-701-12478
; Sequence 12478, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12478
; LENGTH: 1271
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1265_1
US-10-767-701-12478

Query Match      63.6%; Score 14; DB 7; Length 1271;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCCCGAGAACGTAT 19
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Db 832 GCCCGAGAACGTAT 845
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RESULT 9
US-09-404-520B-9481
; Sequence 9481, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emmericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 9481
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Emmericella nidulans
US-09-404-520B-9481

Query Match      63.6%; Score 14; DB 5; Length 1379;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGAGACGTATTCA 22
   |||||
Db 1096 CGAGACGTATTCA 1109

RESULT 10
US-09-404-520B-20466
; Sequence 20466, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emmericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 20466
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Emmericella nidulans
US-09-404-520B-20466

Query Match      63.6%; Score 14; DB 5; Length 1389;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGGCCCGAGAACGT 17
   |||||
Db 365 AGGCCCGAGAACGT 378

RESULT 11
US-10-425-115-166711
; Sequence 166711, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166711
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83619C.1
US-10-425-115-166711

Query Match 63.6%; Score 14; DB 6; Length 1553;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGGCCCGAGAACGT 17
Db 1207 AGGCCCGAGAACGT 1220

RESULT 12
US-09-404-520B-14910
; Sequence 14910, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 14910
; LENGTH: 1866
; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-14910

Query Match 63.6%; Score 14; DB 5; Length 1866;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGGCCCGAGAACGT 17
Db 424 AGGCCCGAGAACGT 437

RESULT 13
US-10-100-683-2841/c
; Sequence 2841, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11

; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2841
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-2841

Query Match 63.6%; Score 14; DB 7; Length 1959;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCCCGAGAACGTA 18
Db 1223 GGCCCGAGAACGTA 1210

RESULT 14
US-10-745-444-764/c
; Sequence 764, Application US/10745444
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/10/745,444
; CURRENT FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 764
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1997168CT1
; PUBLICATION INFORMATION:
US-10-745-444-764

Query Match 63.6%; Score 14; DB 7; Length 2307;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-10-501-933-4270
; Sequence 4270, Application US/10501933
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-01-WO
; CURRENT APPLICATION NUMBER: US/10/501,933
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880

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; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; PRIOR FILING DATE: 2001-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4295
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4270
; LENGTH: 2783
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X83231
US-10-501-933-4270

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	22	100.0	336	1	PCT-US03-03202-2
4	22	100.0	336	1	PCT-US03-03202A-2
5	22	100.0	336	35	US-09-860-200D-2
6	22	100.0	368	3	US-07-323-871B-36
7	22	100.0	370	3	US-07-323-871B-35
8	22	100.0	498	3	US-07-323-871B-1
9	22	100.0	505	3	US-07-323-871-1
10	22	100.0	505	3	US-07-323-871A-1
11	22	100.0	1014	44	US-10-061-071-94
12	22	100.0	1377	23	US-09-548-998A-2
13	22	100.0	1377	23	US-09-548-998A-4
14	22	100.0	1377	23	US-09-548-998A-5
15	22	100.0	1377	23	US-09-548-998A-6
16	22	100.0	1377	23	US-09-548-998C-2
17	22	100.0	1377	23	US-09-548-998C-4
18	22	100.0	1377	23	US-09-548-998C-5
19	22	100.0	1377	23	US-09-548-998C-6
20	22	100.0	1377	23	US-09-548-998E-2
21	22	100.0	1377	23	US-09-548-998E-4
22	22	100.0	1377	23	US-09-548-998E-5
23	22	100.0	1377	23	US-09-548-998E-6
24	22	100.0	1377	44	US-10-061-071-2
25	22	100.0	1377	44	US-10-061-071-4
26	22	100.0	1377	44	US-10-061-071-5
27	22	100.0	1377	44	US-10-061-071-6
28	22	100.0	1378	23	US-09-548-998A-3
29	22	100.0	1378	23	US-09-548-998C-3
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31	22	100.0	1378	23	US-10-061-071-3
32	22	100.0	1443	23	US-09-548-998A-7
33	22	100.0	1443	23	US-09-548-998C-7
34	22	100.0	1443	23	US-09-548-998E-7
35	22	100.0	1443	44	US-10-061-071-7
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37	22	100.0	1451	32	US-09-786-253-5
38	22	100.0	116217	1	PCT-US98-12764-2
39	22	100.0	116217	34	US-09-830-228-2
40	22	100.0	910715	1	PCT-US98-12764-1
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42	22	100.0	1230025	48	US-10-289-762-1
43	22	100.0	1230230	20	US-09-438-185-1
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45	21	95.5	1555893	12	US-08-895-611-1

OTHER INFORMATION: synthetic amplification primer

US-09-940-860-3

Query Match 100.0%; Score 22; DB 39; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTCA 22
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Db 1 ACAAGGCCCGAGAACGTATTCA 22
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RESULT 2

PCT-US01-16030A-2/c
; Sequence 2, Application PC/TUS0116030A
; GENERAL INFORMATION:
; APPLICANT: University of Maryland Biotechnology Institute
; APPLICANT: Sowers, Kevin R.
; TITLE OF INVENTION: May, Harold D.
; TITLE OF INVENTION: Biphenvl Compounds
; FILE REFERENCE: 4115-149 PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16030A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,818
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/266,650
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
PCT-US01-16030A-2

Query Match 100.0%; Score 22; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTCA 22
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Db 323 ACAAGGCCCGAGAACGTATTCA 302
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RESULT 3

PCT-US03-03202-2/c
; Sequence 2, Application PC/TUS0303202
; GENERAL INFORMATION:
; APPLICANT: University of Maryland Biotechnology Institute
; TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Biphen
; FILE REFERENCE: 4115-176 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/03202
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/353,134
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
PCT-US03-03202-2

Query Match 100.0%; Score 22; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1

US-09-940-860-3

Sequence 3, Application US/09940860

GENERAL INFORMATION:

APPLICANT: Rotiman, Richard

APPLICANT: Majumdar, Maulik

TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

FILE REFERENCE: 01107.00185

CURRENT APPLICATION NUMBER: US/09/940, 860

CURRENT FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/229, 376

PRIOR FILING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

QY 1 ACAAGGCCCGAGACGTATTC A 22
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Db 323 ACAAGGCCCGAGACGTATTC A 302

RESULT 4

PCT-US03-03202A-2/c
; Sequence 2, Application PC/TUS0303202A
; GENERAL INFORMATION:
; APPLICANT: University of Maryland Biotechnology Institute
; TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Biphenyls
; FILE REFERENCE: 4115-176 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/03202A
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/353,134
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
PCT-US03-03202A-2

Query Match 100.0%; Score 22; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTC A 22
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Db 323 ACAAGGCCCGAGACGTATTC A 302

RESULT 5

US-09-860-200D-2/c
; Sequence 2, Application US/09860200D
; GENERAL INFORMATION:
; APPLICANT: Kevin, Bowers R.
; APPLICANT: Harold, May D.
; TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of Polychlorinated Biphenyl Compounds
; FILE REFERENCE: 4115-149
; CURRENT APPLICATION NUMBER: US/09/860,200D
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/205,818
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/266,650
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-860-200D-2

Query Match 100.0%; Score 22; DB 35; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 323 ACAAGGCCCGAGACGTATTC A 302

RESULT 6

US-07-923-871B-36/c
; Sequence 36, Application US/07923871B

; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/923,871B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-923-871B-36

Query Match 100.0%; Score 22; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 35, Application US/07923871B
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/923,871B
; FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 489,676
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-923-871B-35

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RESULT 8

```

US-07-923-871B-1/c
; Sequence 1, Application US/07923871B
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,871B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (35..36)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (67)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (164..165)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (167)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: complement (169)
; US-07-923-871B-1

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 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 396 ACAAGGCCCGAGAACGTATTCA 375

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RESULT 9

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US-07-923-871-1/c
; Sequence 1, Application US/07923871
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,871
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 522-1285
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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ANTI-SENSE: NO
FEATURE:
NAME/KEY: unsure
LOCATION: complement (35..36)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (41)
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NAME/KEY: unsure
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FEATURE:
NAME/KEY: unsure
LOCATION: complement (169)
US-07-923-871-1
Query Match 100.0%; Score 22; DB 3; Length 505;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAAGGCCCGAGACGTATTCA 22
DB 396 ACAAGGCCCGAGACGTATTCA 375
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RESULT 10
US-07-923-871A-1/c
Sequence 1, Application US/07923871A
GENERAL INFORMATION:
APPLICANT: White Ph.D, Thomas J.
APPLICANT: Dodge, Deborah E.
TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,871A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 522-1285
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ANTI-SENSE: NO
FEATURE:
NAME/KEY: unsure
LOCATION: complement (35..36)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (41)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (67)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (164..165)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (167)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (169)
US-07-923-871A-1
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Query Match 100.0%; Score 22; DB 3; Length 505;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAAGGCCCGAGACGTATTCA 22
DB 396 ACAAGGCCCGAGACGTATTCA 375
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RESULT 11
US-10-061-071-94/c
Sequence 94, Application US/10061071
GENERAL INFORMATION:
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Microsoft Office 97
SEQ ID NO 94
LENGTH: 1014
TYPE: DNA
ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94
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Query Match 100.0%; Score 22; DB 44; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAAGGCCCGAGACGTATTCA 22
DB 1004 ACAAGGCCCGAGACGTATTCA 983
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RESULT 12
US-09-548-998A-2/c
Sequence 2, Application US/09548998A
GENERAL INFORMATION:
APPLICANT: Ebersole, Richard C.
APPLICANT: Hendrickson, Edwin
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: BC1002 US NA
CURRENT APPLICATION NUMBER: US/09/548,998A
CURRENT FILING DATE: 2001-09-10
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 199.06 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-3

Perfect score: 22
Sequence: 1 acaagcccgagacgtattca 22

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	11	US-09-940-860-3
2	22	100.0	336	10	US-09-860-200D-2
3	22	100.0	1014	15	US-10-061-071-94
4	22	100.0	1377	15	US-10-061-071-2
5	22	100.0	1377	15	US-10-061-071-4
6	22	100.0	1377	15	US-10-061-071-5
7	22	100.0	1377	15	US-10-061-071-6
8	22	100.0	1378	15	US-10-061-071-3
9	22	100.0	1443	15	US-10-061-071-7
10	22	100.0	1230025	16	US-10-289-762-1
11	16	72.7	244	17	US-10-391-249-16
12	16	72.7	354	17	US-10-391-249-17
13	16	72.7	354	17	US-10-391-249-18
14	16	72.7	683	14	US-10-053-078-1

c 15	16	72.7	683	14	US-10-053-078-2	Sequence 2, Appli
c 16	16	72.7	1385	15	US-10-061-071-95	Sequence 95, Appli
c 17	16	72.7	105184	10	US-09-847-513A-1	Sequence 1, Appli
c 18	16	72.7	580073	15	US-10-205-220-1	Sequence 1, Appli
c 19	15	68.2	238484	13	US-10-087-192-544	Sequence 544, App
20	14	63.6	376	14	US-10-040-739-677	Sequence 677, App
21	14	63.6	417	16	US-10-393-840-230	Sequence 230, App
22	14	63.6	450	16	US-10-393-840-229	Sequence 229, App
23	14	63.6	457	10	US-09-918-995-32220	Sequence 32220, A
24	14	63.6	460	10	US-09-918-995-26732	Sequence 26732, A
25	14	63.6	472	15	US-10-066-543-2939	Sequence 2939, Ap
26	14	63.6	506	16	US-10-393-840-227	Sequence 227, App
27	14	63.6	511	10	US-09-918-995-38009	Sequence 38009, A
28	14	63.6	942	13	US-09-942-025-8	Sequence 8, Appli
c 29	14	63.6	1032	9	US-09-974-300-2328	Sequence 2328, Ap
30	14	63.6	1071	10	US-09-933-767-118	Sequence 118, App
31	14	63.6	1071	13	US-10-004-860-118	Sequence 118, App
32	14	63.6	1071	15	US-10-023-283-118	Sequence 118, App
33	14	63.6	1443	13	US-10-425-114-30504	Sequence 30504, A
34	14	63.6	1602	16	US-10-369-493-40891	Sequence 40891, A
35	14	63.6	5469	9	US-09-764-877-4009	Sequence 4009, Ap
36	14	63.6	5469	10	US-09-764-891-9371	Sequence 9371, Ap
37	14	63.6	5469	15	US-10-205-428-817	Sequence 817, App
38	14	63.6	5469	16	US-10-242-515-4000	Sequence 4000, Ap
39	14	63.6	9453	9	US-09-764-877-3999	Sequence 3999, Ap
40	14	63.6	9453	10	US-09-764-891-9370	Sequence 9370, Ap
41	14	63.6	9453	15	US-10-205-428-816	Sequence 816, App
42	14	63.6	9453	16	US-10-242-515-3999	Sequence 3999, Ap
c 43	14	63.6	35178	15	US-10-017-161-739	Sequence 739, App
c 44	14	63.6	46675	13	US-10-087-192-1255	Sequence 1255, Ap
c 45	14	63.6	67311	13	US-09-942-025-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-940-860-3
; Sequence 3, Application US/09940860
; Publication No. US2004000555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majumdar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-3

Query Match 100.0%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGCCCGAGAACGTATTCA 22
|||||
Db 1 ACAAGCCCGAGAACGTATTCA 22

RESULT 2
US-09-860-200D-2/c
; Sequence 2, Application US/09860200D
; Publication No. US20030134408A1
; GENERAL INFORMATION:

APPLICANT: Kevin, Bowers R.
APPLICANT: Harold, May D.
TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of
POLYCHLORINATED BIPHENYL COMPOUNDS
FILE REFERENCE: 4115-149
CURRENT APPLICATION NUMBER: US/09/860,200
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 60/205,818
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/266,650
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 336
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-09-860-200D-2

Query Match 100.0%; Score 22; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGACGTATTCA 22
Db 323 ACAAGGCCCGAGACGTATTCA 302

RESULT 3
US-10-061-071-94/c
Sequence 94, Application US/10061071
Publication No. US20030077601A1
GENERAL INFORMATION:
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Microsoft Office 97
SEQ ID NO 94
LENGTH: 1014
TYPE: DNA
ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94

Query Match 100.0%; Score 22; DB 15; Length 1014;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGACGTATTCA 22
Db 1004 ACAAGGCCCGAGACGTATTCA 983

RESULT 4
US-10-061-071-2/c
Sequence 2, Application US/10061071
Publication No. US20030077601A1
GENERAL INFORMATION:
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
BACTERIA
FILE REFERENCE: BC1002 US CIP

CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 1377
TYPE: DNA
ORGANISM: Dehalococcoides ethenogenes strain PL
US-10-061-071-2

Query Match 100.0%; Score 22; DB 15; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGACGTATTCA 22
Db 1321 ACAAGGCCCGAGACGTATTCA 1300

RESULT 5
US-10-061-071-4/c
Sequence 4, Application US/10061071
Publication No. US20030077601A1
GENERAL INFORMATION:
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 1377
TYPE: DNA
ORGANISM: Dehalococcoides ethenogenes strain DAB
US-10-061-071-4

Query Match 100.0%; Score 22; DB 15; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGACGTATTCA 22
Db 1321 ACAAGGCCCGAGACGTATTCA 1300

RESULT 6
US-10-061-071-5/c
Sequence 5, Application US/10061071
Publication No. US20030077601A1
GENERAL INFORMATION:
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
APPLICANT: HENDRICKSON, EDWIN
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
BACTERIA
FILE REFERENCE: BC1002 US CIP
CURRENT APPLICATION NUMBER: US/10/061,071
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/129,511
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/129,511
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 103

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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Dehalococcoides ethenogenes strain PIN
US-10-061-071-5

Query Match          100.0%; Score 22; DB 15; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAAGGCCCGAGAACGTATTCA 22
        |||||||
DB      1321 ACAAGGCCCGAGAACGTATTCA 1300

RESULT 7
US-10-061-071-6/c
; Sequence 6, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
; APPLICANT: HENDRICKSON, EDWIN
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
; TITLE OF INVENTION: BACTERIA
; FILE REFERENCE: BC1002 US CIP
; CURRENT APPLICATION NUMBER: US/10/061,071
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 60/129,511
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/129,511
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Dehalococcoides ethenogenes strain DLL
US-10-061-071-6

Query Match          100.0%; Score 22; DB 15; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAAGGCCCGAGAACGTATTCA 22
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DB      1321 ACAAGGCCCGAGAACGTATTCA 1300

RESULT 8
US-10-061-071-3/c
; Sequence 3, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
; APPLICANT: HENDRICKSON, EDWIN
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
; TITLE OF INVENTION: BACTERIA
; FILE REFERENCE: BC1002 US CIP
; CURRENT APPLICATION NUMBER: US/10/061,071
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US 60/129,511
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/129,511
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1378
; TYPE: DNA
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US-10-061-071-3

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; NAME/KEY: misc feature
; LOCATION: (675001)..(690000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
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Query Match 100.0%; Score 22; DB 16; Length 1230025;

Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ACAAGGCCCGAGAACGTATTCA 22
      |||||
Db 1012085 ACAAGGCCCGAGAACGTATTCA 1012064
```

RESULT 11

US-10-391-249-16/c

; Sequence 16, Application US/10391249

; Publication No. US20040091935A1

; GENERAL INFORMATION:

; APPLICANT: Dosey, Stephen J.

; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS

; FILE REFERENCE: 07917-142001

; CURRENT APPLICATION NUMBER: US/10/391,249

; CURRENT FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: US 60/364,801

; PRIOR FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-391-249-16

Query Match 72.7%; Score 16; DB 17; Length 244;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 7 CCCGAGAACGTATTCA 22
      |||||
Db 201 CCCGAGAACGTATTCA 186
```

RESULT 12

US-10-391-249-17/c

; Sequence 17, Application US/10391249

; Publication No. US20040091935A1

```
; GENERAL INFORMATION:
; APPLICANT: Dosey, Stephen J.
; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
; FILE REFERENCE: 07917-142001
; CURRENT APPLICATION NUMBER: US/10/391,249
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,801
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-391-249-17
```

Query Match 72.7%; Score 16; DB 17; Length 354;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 7 CCCGAGAACGTATTCA 22
      |||||
Db 299 CCCGAGAACGTATTCA 284
```

RESULT 13

US-10-391-249-18/c

; Sequence 18, Application US/10391249

; Publication No. US20040091935A1

; GENERAL INFORMATION:

; APPLICANT: Dosey, Stephen J.

; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS

; FILE REFERENCE: 07917-142001

; CURRENT APPLICATION NUMBER: US/10/391,249

; CURRENT FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: US 60/364,801

; PRIOR FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Sus scrofa

US-10-391-249-18

Query Match 72.7%; Score 16; DB 17; Length 354;

Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 7 CCCGAGAACGTATTCA 22
      |||||
Db 299 CCCGAGAACGTATTCA 284
```

RESULT 14

US-10-053-078-1/c

; Sequence 1, Application US/10053078

; Publication No. US20020192672A1

; GENERAL INFORMATION:

; APPLICANT: Dawson, Jacqueline E.

; TITLE OF INVENTION: Identification of a New Ehrlichia

; FILE REFERENCE: 6395-62149

; CURRENT APPLICATION NUMBER: US/10/053,078

; CURRENT FILING DATE: 2002-01-17

; PRIOR APPLICATION NUMBER: U.S. 09/061770

; PRIOR FILING DATE: 1998-04-16

; PRIOR APPLICATION NUMBER: U.S. 07/687,526

; PRIOR FILING DATE: 1991-04-18

; PRIOR APPLICATION NUMBER: U.S. 08/147,891

; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: U.S. 08/394,464
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: U.S. 08/943,464
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Ehrlichia chaffeensis
US-10-053-078-1

Query Match 72.7%; Score 16; DB 14; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGAGAGACGTATTCA 22
|||||
Db 579 CCGAGAGACGTATTCA 564

RESULT 15
US-10-053-078-2/c
; Sequence 2, Application US/10053078
; Publication No. US20020192672A1
; GENERAL INFORMATION:
; APPLICANT: Dawson, Jacqueline E.
; APPLICANT: Anderson, Burt
; TITLE OF INVENTION: Identification of a New Ehrlichia
; TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis
; FILE REFERENCE: 6395-62149
; CURRENT APPLICATION NUMBER: US/10/053,078
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: U.S. 09/061770
; PRIOR FILING DATE: 1998-04-16
; PRIOR APPLICATION NUMBER: U.S. 07/687,526
; PRIOR FILING DATE: 1991-04-18
; PRIOR APPLICATION NUMBER: U.S. 08/147,891
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: U.S. 08/394,464
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: U.S. 08/943,464
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 683
; TYPE: DNA
; ORGANISM: E. Canis
US-10-053-078-2

Query Match 72.7%; Score 16; DB 14; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGAGAGACGTATTCA 22
|||||
Db 579 CCGAGAGACGTATTCA 564

Search completed: August 4, 2004, 11:56:26
Job time: 201.06 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 180.771 Seconds

(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-3

Perfect score: 22

Sequence: 1 acaagcccgagacgtattcca 22

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: Geneseq2001as:*
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6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	100.0	336	6 AAD37948	Aad37948 16S ribos
C 2	22	100.0	336	9 AAD58507	Aad58507 16S ribos
C 3	22	100.0	1014	8 AAD58049	Aad58049 Dehalococ
C 4	22	100.0	1284	4 AAH28398	Aah28398 Interengi
C 5	22	100.0	1284	4 AAH28396	Aah28396 Interengi
C 6	22	100.0	1284	4 AAH28401	Aah28401 Interengi
C 7	22	100.0	1284	4 AAH28397	Aah28397 Interengi
C 8	22	100.0	1284	4 AAH28399	Aah28399 Interengi
C 9	22	100.0	1335	4 AAC62240	Aac62240 A 16S rDN
C 10	22	100.0	1377	8 AAD57959	Aad57959 Dehalococ
C 11	22	100.0	1377	8 AAD57957	Aad57957 Dehalococ
C 12	22	100.0	1377	8 AAD57961	Aad57961 Dehalococ
C 13	22	100.0	1377	8 AAD57960	Aad57960 Dehalococ
C 14	22	100.0	1378	8 AAD57958	Aad57958 Dehalococ
C 15	22	100.0	1443	4 AAC62244	Aac62244 A 16S rDN
C 16	22	100.0	1443	8 AAD57962	Aad57962 Dehalococ
C 17	22	100.0	1451	4 AAF31090	Aaf31090 Bacterial
C 18	22	100.0	1451	4 AAF31089	Aaf31089 Bacterial
C 19	22	100.0	1479	6 ABS71617	AbS71617 Rickettsi
C 20	22	100.0	1515	6 ABS71618	AbS71618 Borrelia
C 21	22	100.0	110000	2 AAX20248_04	Continuation (5 of
C 22	22	100.0	110000	2 AAX91990_10	Continuation (11 o
C 23	22	100.0	116277	2 AAX20249	Aax20249 Borrelia

ALIGNMENTS

RESULT 1

AAD37948/c

ID AAD37948 standard; DNA; 336 BP.

XX AC AAD37948;

XX DT 10-SEP-2002 (first entry)

XX DE 16S ribosomal DNA (rDNA) #2.

XX KW Bioremediative microorganism; 16S ribosomal subunit; dechlorination; PCB;

XX KW polychlorinated biphenyl; biodegradation; halogenated organic waste;

XX KW contaminated soil; leachate; aqueous surfactant solution; ds.

XX OS Unidentified.

XX PN WO200189729-A2.

XX PD 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016030.

XX PR 19-MAY-2000; 2000US-0205818P.

XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX Sowers KR, May HD;

XX WPI; 2002-114266/15.

XX Bioremediative microorganism for dechlorinating chlorinated biphenyls and for bioremediation, comprises a specific 16S ribosomal subunit nucleic acid sequence.

XX Claim 1; Fig 22; 102pp; English.

XX The present invention relates to bioremediative microorganisms comprising the 16S ribosomal subunit nucleic acid sequence. The microorganisms of the invention are useful for dechlorinating polychlorinated biphenyls (PCBs) including anaerobic dechlorination of ortho- and double-flanked chloro substituents of PCBs. They are useful for biodegradation of halogenated organic waste, e.g., contaminated soil from landfill sites and river beds containing PCBs and to treat leachates and aqueous surfactant solutions resulting from washing the organic waste to transfer PCBs to the aqueous surfactant solutions. The method of the invention is useful for

Aaq36494 Mycoplasma
Aaq36491 Mycoplasma
Aaq36493 Mycoplasma
Aaq36490 Mycoplasma
Aaq36495 Mycoplasma
Aaq21032 Region sp
Aaq21034 Region sp
Aaq21035 Region sp
Aaq15188 Ehrlichia
Aav43697 Ehrlichia
Ada18591 E. canis
Ada18587 E. chaffe
Acd26696 Ehrlichia
Acd26697 Ehrlichia
Abx93090 DNA seque
Abx93091 DNA seque
Aax61135 P36 ribos
Aax61134 P36 ribos
Aad58050 Dehalococ
Abz79794 Mycoplasma
Abz79792 Mycoplasma
Abz79793 Mycoplasma

CC determining the bioremediative potential of CB-containing site, which is
 CC useful for monitoring CB-containing site. The invention also relates to
 CC compositions which are useful for bioremediation. The present sequence is
 CC a 16S ribosomal DNA (rDNA) of the invention

SQ Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;
 Query Match 100.0%; Score 22; DB 6; Length 336;
 Best Local Similarity 100.0%; Pred. No. 0.00072;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACAAGGCCGAGAACGTATTCA 22
 |||||
 DB 323 ACAAGGCCGAGAACGTATTCA 302

RESULT 2

AAD58507/c
 ID AAD58507 standard; DNA; 336 BP.

AC AAD58507;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX 16S ribosomal subunit DNA #2.
 DE
 XX Polychlorinated biphenyls; PCBs; dechlorinating activity; ds.
 KW
 XX Unidentified.
 OS
 XX WO2003065011-A2.
 PN
 XX 07-AUG-2003.
 PD
 XX
 XX 03-FEB-2003; 2003WO-US003202.
 PF
 XX
 XX 01-FEB-2002; 2002US-0353134P.
 PR
 XX (UTMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 PA
 XX Sowers KR, May HD;
 PI
 XX WPI; 2003-636818/60.
 DR
 XX

STimulation of polychlorinated biphenyl dechlorinating bacteria comprises
 contacting polychlorinated biphenyl dechlorinating bacteria with
 stimulant having polyhalogenated ethene(s).

PS Disclosure; Fig 4; 4lpp; English.

XX The present invention relates to compositions and methods for
 CC bioremediation of polychlorinated biphenyls (PCBs) using dechlorinating
 CC microorganisms grown in the presence of stimulating halogenated
 CC hydrocarbons and polyhalogenated ethenes. Polyhalogenated ethenes are
 CC used to stimulate the growth and dechlorinating activity of PCB
 CC dechlorinating bacteria in a contaminated soil or sediment. The present
 CC sequence is 16S ribosomal subunit DNA

SQ Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 9; Length 336;
 Best Local Similarity 100.0%; Pred. No. 0.00072;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACAAGGCCGAGAACGTATTCA 22
 |||||
 DB 323 ACAAGGCCGAGAACGTATTCA 302

RESULT 3

AAD58049/c
 ID AAD58049 standard; DNA; 1014 BP.

XX

AC AAD58049;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Dehalococcoides related family A 16S DHFA sequence.
 DE
 XX 16S rDNA; dechlorinating bacterial organism; ds.
 KW
 XX Unidentified.
 OS
 XX WO2003064695-A1.
 PN
 XX 07-AUG-2003.
 PD
 XX
 XX 30-JAN-2002; 2002WO-US003927.
 PF
 XX
 XX 30-JAN-2002; 2002WO-US003927.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Ebersole R, Hendrickson E;
 PI
 XX WPI; 2003-636804/60.
 DR
 XX

Novel isolated 16S rDNA sequence useful for forming probes and primers
 PT which are useful for identifying dechlorinating bacterial organism in
 PT various samples.

XX Claim 1; Page 99-100; 110pp; English.

CC The invention relates to an isolated 16S rDNA sequence indicative of a
 CC dechlorinating bacterial organism. The invention is useful for forming
 CC probes and primers which are useful for identifying dechlorinating
 CC bacterial organism in various samples. The method of the invention is
 CC useful for identifying a dechlorinating bacterial organism that is a
 CC member of a cell population or consortium. The isolated bacterial
 CC organism is useful for dechlorinating chlorinated compounds which
 CC involves contacting a chlorinated compound with the organism.
 CC Oligonucleotide polymer of the invention is useful for separating sub-
 CC families of dechlorinating bacterial organism. The present sequence is
 CC Dehalococcoides related family A 16S DHFA sequence

SQ Sequence 1014 BP; 256 A; 238 C; 309 G; 211 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 0.0007;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACAAGGCCGAGAACGTATTCA 22
 |||||
 DB 1004 ACAAGGCCGAGAACGTATTCA 983

RESULT 4

AAH28398/c
 ID AAH28398 standard; rRNA; 1284 BP.

XX AAH28398;

XX 11-SEP-2003 (revised)

DT 17-SEP-2001 (first entry)

XX Intergenic spacer between 16S and 23S rRNA genes of strain FML-12.

XX Intergenic spacer; Chlamydiaeae; 16S rRNA; 23S rRNA; Region A; Region B;
 KW chlamydial infection; ss.

XX Chlamydia pneumoniae.

XX Key Location/Qualifiers

FT misc_RNA 1-537 b

FT /tag= "Region A"
 FT /note= "Region A"

```

FT rRNA      1. .221
FT /*tag= a
FT /note= "16S rRNA"
FT misc_RNA  222. .444
FT /*tag= c
FT /*note= "intergenic spacer"
FT rRNA      445. .1284
FT /*tag= e
FT /*note= "23S rRNA"
FT rRNA      445. .1063
FT /*tag= d
FT /*note= "Domain I of 23S rRNA"
FT misc_RNA  959. .1086
FT /*tag= f
FT /*note= "Region B"
FT FT
FT XX
XX US6261769-B1.
XX PN
XX 17-JUL-2001.
XX PD
XX 31-MAR-1998; 98US-00052333.
XX PF
XX 31-MAR-1998; 98US-00052333.
XX PR
XX (USDA ) US SEC OF AGRIC.
XX PA
XX Everett KDE, Andersen AA;
XX PI
XX WPI; 2001-440857/47.
XX DR
XX New primers and probes derived from sequences of intergenic spacer
XX between 16S and 23S genes and region of Domain I in 23S region of
XX Chlamydiaeae, useful for assaying and identifying all strains of
XX Chlamydiaeae.
XX PS
XX Disclosure; Col 119-120; 89pp; English.
XX AAH28371-AAH28413 represent intergenic spacer target sequences, derived
XX from Chlamydiaeae. The sequences comprise the intergenic spacer between
XX the 16S and the 23S rRNA genes, including the far downstream end of the
XX 16S and the far upstream end of the 23S domain I flanking intergenic
XX spacer (referred to as Region A), and secondarily, a 131 bp region in the
XX 3' end of Domain I (referred to as Region B). The sequences provide
XX suitable target sequences for developing probes and primers which are
XX useful for identifying and detecting Chlamydiaeae. The primers and
XX probes can be used to identify the presence of Chlamydiaeae in a test
XX sample, or to distinguish one strain from another, and for diagnosing
XX chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX CC
XX Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 4; Length 1284;
XX Best Local Similarity 100.0%; Pred NO. 0.00069;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACAAGGCCCGAGAACGTATTCA 22
XX |||||
XX Db 67 ACAAGGCCCGAGAACGTATTCA 46

RESULT 5
AAH28396/c
ID AAH28396 standard; rRNA; 1284 BP.
XX
XX AAH28396;
XX AC
XX 11-SEP-2003 (revised)
XX DT 17-SEP-2001 (first entry)
XX DE
XX Intergenic spacer between 16S and 23S rRNA genes of strain CWL-029.
XX Intergenic spacer; Chlamydiaeae; 16S rRNA; 23S rRNA; Region A; Region B;
XX KW

```

```

KW chlamydial infection; ss.
XX OS
XX Chlamydia pneumoniae.
XX FH
XX Key Location/Qualifiers
XX misc_RNA 1. .537
XX /*tag= b
XX /note= "Region A"
XX rRNA 1. .221
XX /*tag= a
XX /note= "16S rRNA"
XX misc_RNA 222. .444
XX /*tag= c
XX /note= "intergenic spacer"
XX rRNA 445. .1284
XX /*tag= e
XX /note= "23S rRNA"
XX rRNA 445. .1063
XX /*tag= d
XX /note= "Domain I of 23S rRNA"
XX misc_RNA 959. .1086
XX /*tag= f
XX /note= "Region B"
XX US6261769-B1.
XX PN
XX 17-JUL-2001.
XX PD
XX 31-MAR-1998; 98US-00052333.
XX PF
XX 31-MAR-1998; 98US-00052333.
XX PR
XX (USDA ) US SEC OF AGRIC.
XX PA
XX Everett KDE, Andersen AA;
XX PI
XX WPI; 2001-440857/47.
XX DR
XX New primers and probes derived from sequences of intergenic spacer
XX between 16S and 23S genes and region of Domain I in 23S region of
XX Chlamydiaeae, useful for assaying and identifying all strains of
XX Chlamydiaeae.
XX PS
XX Disclosure; Col 113-116; 89pp; English.
XX AAH28371-AAH28413 represent intergenic spacer target sequences, derived
XX from Chlamydiaeae. The sequences comprise the intergenic spacer between
XX the 16S and the 23S rRNA genes, including the far downstream end of the
XX 16S and the far upstream end of the 23S domain I flanking intergenic
XX spacer (referred to as Region A), and secondarily, a 131 bp region in the
XX 3' end of Domain I (referred to as Region B). The sequences provide
XX suitable target sequences for developing probes and primers which are
XX useful for identifying and detecting Chlamydiaeae. The primers and
XX probes can be used to identify the presence of Chlamydiaeae in a test
XX sample, or to distinguish one strain from another, and for diagnosing
XX chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
XX standardise OS field)
XX CC
XX Sequence 1284 BP; 394 A; 218 C; 329 G; 343 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 22; DB 4; Length 1284;
XX Best Local Similarity 100.0%; Pred. No. 0.00069;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ACAAGGCCCGAGAACGTATTCA 22
XX |||||
XX Db 67 ACAAGGCCCGAGAACGTATTCA 46

RESULT 6
AAH28401/c
ID AAH28401 standard; rRNA; 1284 BP.
XX

```

AAH28401;
 11-SEP-2003 (revised)
 17-SEP-2001 (first entry)
 Intergerenic spacer between 16S and 23S rRNA genes of strain TW-183.
 Intergerenic spacer; Chlamydiae; 16S rRNA; 23S rRNA; Region A; Region B;
 chlamydial infection; ss.
 Chlamydia pneumoniae.
 Key Location/Qualifiers
 misc_RNA 1..537
 /tag= b
 /note= "Region A"
 rRNA 1..221
 /tag= a
 /note= "16S rRNA"
 misc_RNA 222..444
 /tag= c
 /note= "intergenic spacer"
 rRNA 445..1284
 /tag= e
 /note= "23S rRNA"
 rRNA 445..1063
 /tag= d
 /note= "Domain I of 23S rRNA"
 misc_RNA 959..1086
 /tag= f
 /note= "Region B"
 US6261769-B1.
 17-JUL-2001.
 31-MAR-1998; 98US-00052333.
 31-MAR-1998; 98US-00052333.
 (USDA) US SEC OF AGRIC.
 Everett KDE, Andersen AA;
 WPI; 2001-440857/47.
 New primers and probes derived from sequences of intergenic spacer
 between 16S and 23S genes and region of Domain I in 23S region of
 Chlamydiae, useful for assaying and identifying all strains of
 Chlamydiae.
 Disclosure; Col 125-128; 89pp; English.
 AAH28371-AAH28413 represent intergenic spacer target sequences, derived
 from Chlamydiae. The sequences comprise the intergenic spacer between
 the 16S and the 23S rRNA genes, including the far downstream end of the
 16S and the far upstream end of the 23S domain I flanking intergenic
 spacer (referred to as Region A), and secondarily, a 131 bp region in the
 3' end of Domain I (referred to as Region B). The sequences provide
 suitable target sequences for developing probes and primers which are
 useful for identifying and detecting Chlamydiae. The primers and
 probes can be used to identify the presence of Chlamydiae in a test
 sample, or to distinguish one strain from another, and for diagnosing
 chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
 standardise OS field)
 Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;
 Query Match 100.0%; Score 22; DB 4; Length 1284;
 Best Local Similarity 100.0%; Pred. No. 0.00069;
 *Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ACAAGGCCGAGACGTATTCA 22

Db 67 ACAAGGCCGAGACGTATTCA 46
 RESULT 7
 AAH28397/c
 ID AAH28397 standard; rRNA; 1284 BP.
 XX AC AAH28397;
 XX DT 11-SEP-2003 (revised)
 XX DT 17-SEP-2001 (first entry)
 XX DE Intergerenic spacer between 16S and 23S rRNA genes of strain CWL-1011.
 XX KW Intergerenic spacer; Chlamydiae; 16S rRNA; 23S rRNA; Region A; Region B;
 KW chlamydial infection; ss.
 XX OS Chlamydia pneumoniae.
 XX FH Key Location/Qualifiers
 FT misc_RNA 1..537
 /tag= b
 /note= "Region A"
 FT rRNA 1..221
 /tag= a
 /note= "16S rRNA"
 FT misc_RNA 222..444
 /tag= c
 /note= "intergenic spacer"
 FT rRNA 445..1284
 /tag= e
 /note= "23S rRNA"
 FT rRNA 445..1063
 /tag= d
 /note= "Domain I of 23S rRNA"
 FT misc_RNA 959..1086
 /tag= f
 /note= "Region B"
 XX US6261769-B1.
 XX 17-JUL-2001.
 XX 31-MAR-1998; 98US-00052333.
 XX 31-MAR-1998; 98US-00052333.
 XX (USDA) US SEC OF AGRIC.
 XX Everett KDE, Andersen AA;
 XX WPI; 2001-440857/47.
 XX New primers and probes derived from sequences of intergenic spacer
 between 16S and 23S genes and region of Domain I in 23S region of
 Chlamydiae, useful for assaying and identifying all strains of
 Chlamydiae.
 XX Disclosure; Col 115-118; 89pp; English.
 AAH28371-AAH28413 represent intergenic spacer target sequences, derived
 from Chlamydiae. The sequences comprise the intergenic spacer between
 the 16S and the 23S rRNA genes, including the far downstream end of the
 16S and the far upstream end of the 23S domain I flanking intergenic
 spacer (referred to as Region A), and secondarily, a 131 bp region in the
 3' end of Domain I (referred to as Region B). The sequences provide
 suitable target sequences for developing probes and primers which are
 useful for identifying and detecting Chlamydiae. The primers and
 probes can be used to identify the presence of Chlamydiae in a test
 sample, or to distinguish one strain from another, and for diagnosing
 chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
 standardise OS field)

```

XX Sequence 1284 BP; 392 A; 218 C; 331 G; 343 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 22; DB 4; Length 1284;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTCA 22
DB 67 ACAAGGCCCGAGAACGTATTCA 46

RESULT 8
AAH28399/c
ID AAH28399 standard; rRNA; 1284 BP.
XX
AC AAH28399;
XX
DT 11-SEP-2003 (revised)
DT 17-SEP-2001 (first entry)
XX
Intergenic spacer between 16S and 23S rRNA genes of strain FVL-16.
XX
Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW chlamydial infection; ss.
XX
OS Chlamydothilla pneumoniae.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..537
FT /*tag= b
FT /note= "Region A"
FT rRNA 1..221
FT /*tag= a
FT /note= "16S rRNA"
FT misc_RNA 222..444
FT /*tag= c
FT /note= "intergenic spacer"
FT rRNA 445..1284
FT /*tag= e
FT /note= "23S rRNA"
FT rRNA 445..1063
FT /*tag= d
FT /note= "Domain I of 23S rRNA"
FT misc_RNA 959..1086
FT /*tag= f
FT /note= "Region B"
XX
US6261769-B1.
XX
PD 17-JUL-2001.
XX
PF 31-MAR-1998; 98US-00052333.
XX
PR 31-MAR-1998; 98US-00052333.
XX
PA (USDA ) US SEC OF AGRIC.
XX
PI Everett KDE, Andersen AA;
XX
DR WPI; 2001-440857/47.
XX
New primers and probes derived from sequences of intergenic spacer
PT between 16S and 23S genes and region of Domain I in 23S region of
PT Chlamydiaceae, useful for assaying and identifying all strains of
PT Chlamydiaceae.
XX
PS Disclosure; Col 121-122; 89pp; English.
XX
CC AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC the 16S and the 23S rRNA genes, including the far downstream end of the
CC 16S and the far upstream end of the 23S domain I flanking intergenic

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```

CC spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC 3' end of Domain I (referred to as Region B). The sequences provide
CC suitable target sequences for developing probes and primers which are
CC useful for identifying and detecting Chlamydiaceae. The primers and
CC probes can be used to identify the presence of Chlamydiaceae in a test
CC sample, or to distinguish one strain from another, and for diagnosing
CC chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 1284;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTCA 22
DB 67 ACAAGGCCCGAGAACGTATTCA 46

RESULT 9
AAC62240/c
ID AAC62240 standard; DNA; 1335 BP.
XX
AC AAC62240;
XX
DT 19-MAR-2001 (first entry)
XX
DE A 16S rDNA sequence indicative of a chlorinating bacterial strain.
KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS Dehalococcoides ethenogenes.
XX
FN WO200063443-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009883.
XX
PR 15-APR-1999; 99US-0129511P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Hendrickson ER, Ebersole RC;
XX
DR WPI; 2001-024581/03.
XX
PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT indicative of a dechlorinating bacterial strain.
XX
PS Claim 1; Page 47-48; 55pp; English.
XX
The present sequence represents the 16S rDNA profile of Dehalococcoides
CC ethenogenes strain STF, isolated from soil surrounding an industrial
CC site. The 16S rDNA profile is linked to dechlorinating activity.
CC Bacterial strain comprising the 16S rDNA sequence of the invention are
CC useful for the dechlorination of chlorinated compounds such as
CC carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC trichloroethane, dichloroethylene, vinyl chloride, and chloroformatics.
CC The 16S rDNA sequence is also useful for identification of new
CC chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC ethenogenes
XX
SQ Sequence 1335 BP; 348 A; 288 C; 403 G; 296 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 4; Length 1335;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTCA 22

```

```

Db      1322 ACAAGGCCCGAGAACGTATTC A 1301
|||||
RESULT 10
AAD57957/c
ID      AAD57957 standard; DNA; 1377 BP.
XX
AC      AAD57957;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Dehalococcoides ethenogenes strain DAB 16S rDNA (DHE-DAB) .
XX
KW      16S rDNA; dechlorinating bacterial organism; ds.
XX
OS      Dehalococcoides ethenogenes.
XX
PN      WO2003064695-A1.
XX
PD      07-AUG-2003.
XX
PF      30-JAN-2002; 2002WO-US003927.
XX
PR      30-JAN-2002; 2002WO-US003927.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI      Ebersole R, Hendrickson E;
XX
WPI; 2003-636804/60.
XX
Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS      Claim 31; Fig 1; 110pp; English.
XX
CC      The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ      Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;

Query Match      100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. NO. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 ACAAGGCCCGAGAACGTATTC A 22
|||||
DB      1321 ACAAGGCCCGAGAACGTATTC A 1300

RESULT 11
AAD57957/c
ID      AAD57957 standard; DNA; 1377 BP.
XX
AC      AAD57957;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Dehalococcoides ethenogenes strain PL 16S rDNA (DHE-PL) .
XX
KW      16S rDNA; dechlorinating bacterial organism; ds.
XX
OS      Dehalococcoides ethenogenes.
XX
PN      WO2003064695-A1.
XX
PD      07-AUG-2003.
XX
PF      30-JAN-2002; 2002WO-US003927.
XX
PR      30-JAN-2002; 2002WO-US003927.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI      Ebersole R, Hendrickson E;
XX
WPI; 2003-636804/60.
XX
Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS      Claim 31; Fig 1; 110pp; English.
XX
CC      The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ      Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;

Query Match      100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. NO. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 ACAAGGCCCGAGAACGTATTC A 22
|||||
DB      1321 ACAAGGCCCGAGAACGTATTC A 1300

RESULT 12
AAD57961/c
ID      AAD57961 standard; DNA; 1377 BP.
XX
AC      AAD57961;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Dehalococcoides ethenogenes strain DLL 16S rDNA (DHE-DLL) .
XX
KW      16S rDNA; dechlorinating bacterial organism; ds.
XX
OS      Dehalococcoides ethenogenes.
XX
PN      WO2003064695-A1.
XX
PD      07-AUG-2003.
XX
PF      30-JAN-2002; 2002WO-US003927.
XX
PR      30-JAN-2002; 2002WO-US003927.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI      Ebersole R, Hendrickson E;
XX
WPI; 2003-636804/60.
XX
Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS      Claim 31; Fig 1; 110pp; English.
XX
CC      The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ      Sequence 1377 BP; 361 A; 298 C; 412 G; 305 T; 0 U; 1 Other;

```

PT Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
various samples.

PS Claim 31; Fig 1; 110pp; English.

XX The invention relates to an isolated 16S rDNA sequence indicative of a
XX dechlorinating bacterial organism. The invention is useful for forming
XX probes and primers which are useful for identifying dechlorinating
XX bacterial organism in various samples. The method of the invention is
XX useful for identifying a dechlorinating bacterial organism that is a
XX member of a cell population or consortium. The isolated bacterial
XX organism is useful for dechlorinating chlorinated compounds which
XX involves contacting a chlorinated compound with the organism.
XX Oligonucleotide polymer of the invention is useful for separating sub-
XX families of dechlorinating bacterial organism. The present sequence is
XX Dehalococcoides ethenogenes 16S rDNA

SQ Sequence 1377 BP; 360 A; 300 C; 414 G; 303 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22
DB 1321 ACAAGGCCCGAGACGTATTCA 1300

RESULT 13

AAD57960/c

ID AAD57960 standard; DNA; 1377 BP.

XX

AC AAD57960;

XX 20-NOV-2003 (first entry)

DT

XX Dehalococcoides ethenogenes strain PIN 16S rDNA (DHE-PIN).

DE

XX 16S rDNA; dechlorinating bacterial organism; ds.

KW

XX Dehalococcoides ethenogenes.

OS

XX WO2003064695-A1.

PN

XX 07-AUG-2003.

PD

XX 30-JAN-2002; 2002WO-US003927.

PF

XX 30-JAN-2002; 2002WO-US003927.

PR

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA

XX Ebersole R, Hendrickson E;

PI

XX WPI; 2003-636804/60.

DR

XX Novel isolated 16S rDNA sequence useful for forming probes and primers
XX which are useful for identifying dechlorinating bacterial organism in
various samples.

PT

XX Claim 31; Fig 1; 110pp; English.

PS

XX The invention relates to an isolated 16S rDNA sequence indicative of a
XX dechlorinating bacterial organism. The invention is useful for forming
XX probes and primers which are useful for identifying dechlorinating
XX bacterial organism in various samples. The method of the invention is
XX useful for identifying a dechlorinating bacterial organism that is a
XX member of a cell population or consortium. The isolated bacterial
XX organism is useful for dechlorinating chlorinated compounds which
XX involves contacting a chlorinated compound with the organism.
XX Oligonucleotide polymer of the invention is useful for separating sub-
XX families of dechlorinating bacterial organism. The present sequence is

CC

CC Dehalococcoides ethenogenes 16S rDNA

XX

SQ Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22

DB 1321 ACAAGGCCCGAGACGTATTCA 1300

RESULT 14

AAD57958/c

ID AAD57958 standard; DNA; 1378 BP.

XX

AC AAD57958;

XX

DT 20-NOV-2003 (first entry)

DE

XX Dehalococcoides ethenogenes strain V/SFD 16S rDNA (DHE-V/SFD).

DE

XX 16S rDNA; dechlorinating bacterial organism; ds.

KW

XX Dehalococcoides ethenogenes.

OS

XX WO2003064695-A1.

PN

XX 07-AUG-2003.

PD

XX 30-JAN-2002; 2002WO-US003927.

PF

XX 30-JAN-2002; 2002WO-US003927.

PR

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA

XX Ebersole R, Hendrickson E;

PI

XX WPI; 2003-636804/60.

DR

XX Novel isolated 16S rDNA sequence useful for forming probes and primers
XX which are useful for identifying dechlorinating bacterial organism in
various samples.

PT

XX Claim 31; Fig 1; 110pp; English.

PS

XX The invention relates to an isolated 16S rDNA sequence indicative of a
XX dechlorinating bacterial organism. The invention is useful for forming
XX probes and primers which are useful for identifying dechlorinating
XX bacterial organism in various samples. The method of the invention is
XX useful for identifying a dechlorinating bacterial organism that is a
XX member of a cell population or consortium. The isolated bacterial
XX organism is useful for dechlorinating chlorinated compounds which
XX involves contacting a chlorinated compound with the organism.
XX Oligonucleotide polymer of the invention is useful for separating sub-
XX families of dechlorinating bacterial organism. The present sequence is

CC

CC Dehalococcoides ethenogenes 16S rDNA

XX

SQ Sequence 1378 BP; 361 A; 300 C; 413 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1378;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGACGTATTCA 22

DB 1322 ACAAGGCCCGAGACGTATTCA 1301

RESULT 15

AAC62244/c

ID AAC62244 standard; DNA; 1443 BP.

```

XX AAC62244;
AC
XX
XX DT 19-MAR-2001 (first entry)
XX
XX DE A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
XX KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW carbon tetrachloride; tetrachloroethane; chloroform; dichloromethane;
XX trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
XX OS Dehalococcoides ethenogenes.
XX
XX PN WO200063443-A2.
XX
XX PD 26-OCT-2000.
XX
XX PF 13-APR-2000; 2000WO-US009883.
XX
XX PR 15-APR-1999; 99US-0129511P.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX PI Hendrickson ER, Ebersole RC;
XX
XX DR WPI; 2001-024581/03.
XX
XX PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
XX indicative of a dechlorinating bacterial strain.
XX
XX PS Example 2; Page 49-50; 55pp; English.
XX
XX CC The present sequence represents the 16S rDNA profile of Dehalococcoides
XX ethenogenes strain 195. The 16S rDNA profile is linked to dechlorinating
XX activity. Bacterial strain comprising the 16S rDNA sequence of the
XX invention are useful for the dechlorination of chlorinated compounds such
XX as carbon tetrachloride, tetrachloroethane, chloroform, dichloromethane,
XX trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
XX The 16S rDNA sequence is also useful for identification of new
XX chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
XX ethenogenes
XX
XX SQ Sequence 1443 BP; 379 A; 306 C; 443 G; 314 T; 0 U; 1 Other;
Query Match 100.0%; Score 22; DB 4; Length 1443;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTATTC A 22
Db 1329 ACAAGGCCCGAGAACGTATTC A 1308

Search completed: August 4, 2004, 06:43:37
Job time : 182.771 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 208.988 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-4

Perfect score: 21
Sequence: 1 gtgcagcagcagcggttaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending Patents NA New:**

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- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	81.0	1542	8	US-10-864-684-581
C 2	17	81.0	2838	1	PCT-US03-41761-45189
C 3	17	81.0	2838	1	PCT-US03-41761-45189
C 4	17	81.0	2838	1	PCT-US03-41766A-45189
C 5	16	76.2	783	1	PCT-US03-36229-174
C 6	16	76.2	783	1	PCT-US04-17686-2493
C 7	16	76.2	815	6	US-10-425-115-47421
C 8	16	76.2	830	6	US-10-425-115-79433
C 9	16	76.2	1119	6	US-10-669-143-12
C 10	16	76.2	1119	7	US-10-835-208-10
C 11	16	76.2	1647	1	PCT-US04-05092-48
C 12	16	76.2	10925	7	US-10-767-471-10719
C 13	15	71.4	201	6	US-10-425-115-139088
C 14	15	71.4	213	1	PCT-US04-12047-347
C 15	15	71.4	260	6	US-10-425-115-49000
C 16	15	71.4	300	6	US-10-425-115-44757
C 17	15	71.4	526	6	US-10-425-115-139649
C 18	15	71.4	717	6	US-10-425-115-152690
C 19	15	71.4	748	6	US-10-425-115-171414
C 20	15	71.4	837	6	US-10-425-115-146825
C 21	15	71.4	863	6	US-10-425-115-146920
C 22	15	71.4	923	7	US-10-767-701-11322
C 23	15	71.4	1083	1	PCT-US04-02974-43
C 24	15	71.4	1083	7	US-10-770-668-43

25 15 71.4 1126 1 PCT-US03-41761-34028 Sequence 34028, A
26 15 71.4 1126 1 PCT-US03-41761-34028 Sequence 34028, A
27 15 71.4 1126 1 PCT-US03-41766A-34028 Sequence 34028, A
c 28 15 71.4 1167 1 PCT-US04-07467-211 Sequence 211, App
29 15 71.4 1205 6 US-10-425-115-100996 Sequence 100996,
c 30 15 71.4 1343 6 US-10-425-115-179268 Sequence 179268,
c 31 15 71.4 1636 7 US-10-796-174-56 Sequence 56, Appl
c 32 15 71.4 1739 6 US-10-425-115-14642 Sequence 14642, A
c 33 15 71.4 1751 1 PCT-US04-12706-29 Sequence 29, Appl
c 34 15 71.4 1751 7 US-10-830-828-29 Sequence 29, Appl
c 35 15 71.4 2039 7 US-10-491-468-79 Sequence 79, Appl
c 36 15 71.4 3770 1 PCT-US04-11193-9 Sequence 9, Appl
c 37 15 71.4 3884 6 US-10-127-823A-145 Sequence 145, App
c 38 15 71.4 3884 7 US-10-152-372-145 Sequence 145, App
c 39 15 71.4 3884 7 US-10-123-155-145 Sequence 145, App
c 40 15 71.4 3884 8 US-10-143-117-145 Sequence 145, App
c 41 15 71.4 3884 8 US-10-143-117-145 Sequence 145, App
c 42 15 71.4 5337 7 US-10-852-074-11 Sequence 11, Appl
c 43 15 71.4 17777 8 US-10-868-184A-5663 Sequence 5663, Ap
c 44 15 71.4 17777 8 US-10-868-184-5663 Sequence 5663, Ap
c 45 14 66.7 78 1 PCT-US03-41269-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-864-684-581/c
; Sequence 581, Application US/10864684
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizzia, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/10/864,684
; CURRENT FILING DATE: 2004-06-08
; NUMBER OF SEQ ID NOS: 1168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 581
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-864-684-581

Query Match 81.0%; Score 17; DB 8; Length 1542;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTAA 19
|||||
Db 1148 GCCAGCAGCAGCGGTAA 1132

RESULT 2
PCT-US03-41761-45189/c
; Sequence 45189, Application PC/TUS0341761
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: CHARTERIS, Paul
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
; FILE REFERENCE: MM1150M0
; CURRENT APPLICATION NUMBER: PCT/US03/41761
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 45189
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Bovine 1986680933064
PCT-US03-41761-45189

Query Match      81.0%; Score 17; DB 1; Length 2838;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
Db 2268 GTGCCAGCAGCAGCGGT 2252

RESULT 3
PCT-US03-41761-45189/c
; Sequence 45189, Application PC/TUS0341761
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: CHARTERIS, Paul
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
; FILE REFERENCE: MM1150W0
; CURRENT APPLICATION NUMBER: PCT/US03/41761
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 45189
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Bovine 1986680933064
PCT-US03-41761-45189

Query Match      81.0%; Score 17; DB 1; Length 2838;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
Db 2268 GTGCCAGCAGCAGCGGT 2252

RESULT 4
PCT-US03-41766A-45189/c
; Sequence 45189, Application PC/TUS0341766A
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100W0
; CURRENT APPLICATION NUMBER: PCT/US03/41766A
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 45189
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Bovine 1986680933064
PCT-US03-41766A-45189

Query Match      81.0%; Score 17; DB 1; Length 2838;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
Db 2268 GTGCCAGCAGCAGCGGT 2252

RESULT 5
PCT-US03-36229-174
; Sequence 174, Application PC/TUS0336229
; GENERAL INFORMATION:
; APPLICANT: Nura Inc
; TITLE OF INVENTION: Nuclear Receptor-Based Diagnostic,
; FILE REFERENCE: 50001/014W02
; CURRENT APPLICATION NUMBER: PCT/US03/36229
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/426,305
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US03-36229-174

Query Match      76.2%; Score 16; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
Db 129 GTGCCAGCAGCAGCGG 144

RESULT 6
PCT-US04-17686-2493
; Sequence 2493, Application PC/TUS0417686
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
; APPLICANT: THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
; APPLICANT: FOR DISEASE CONTROL AND PREVENTION
; TITLE OF INVENTION: PNI MICROARRAY AND USES
; FILE REFERENCE: 14114.0375P1
; CURRENT APPLICATION NUMBER: PCT/US04/17686
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/475,915
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 3085
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2493
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-17686-2493

Query Match      76.2%; Score 16; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
Db 129 GTGCCAGCAGCAGCGG 144

RESULT 7
US-10-425-115-47421
; Sequence 47421, Application US/10425115
; GENERAL INFORMATION:
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 47421
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(815)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_143255C.1
US-10-425-115-47421

Query Match          76.2%; Score 16; DB 6; Length 815;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GCCAGCAGCAGCGGTA 18
Db      552 GCCAGCAGCAGCGGTA 567

RESULT 8
US-10-425-115-79433/c
; Sequence 79433, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79433
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172470C.1
US-10-425-115-79433

Query Match          76.2%; Score 16; DB 6; Length 830;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GCCAGCAGCAGCGGTA 18
Db      822 GCCAGCAGCAGCGGTA 807

RESULT 9
US-10-669-143-12
; Sequence 12, Application US/10669143
; GENERAL INFORMATION:
; APPLICANT: William Matthews
; APPLICANT: Mark Moore
; APPLICANT: Russell Phillips
; APPLICANT: Michael V. Wiles
; APPLICANT: Thadd C. Reeder
; APPLICANT: Robert G. Wisotzkey
; APPLICANT: Keith D. Allen
```

```
; APPLICANT: Helen Baribault
; APPLICANT: Thomas J. Brennan
; APPLICANT: Catherine Guenther
; APPLICANT: Robert Klein
; APPLICANT: Christopher J. Kirk
; APPLICANT: Simon X. Xie
; APPLICANT: Qin Zhang
; APPLICANT: Agnes Chopin
; TITLE OF INVENTION: Targeted Gene Disruptions, Compositions
; TITLE OF INVENTION: and Methods Related Thereto
; FILE REFERENCE: R-DB-13
; CURRENT APPLICATION NUMBER: US/10/669,143
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/413,647
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,666
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,653
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,646
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,625
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,639
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; OTHER INFORMATION: US-10-669-143-12

Query Match          76.2%; Score 16; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTGCCAGCAGCAGCGG 16
Db      161 GTGCCAGCAGCAGCGG 176

RESULT 10
US-10-835-208-10
; Sequence 10, Application US/10835208
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: ISPH-0593
; CURRENT APPLICATION NUMBER: US/10/835,208
; CURRENT FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US/09/919,197
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(815)
US-10-835-208-10

Query Match          76.2%; Score 16; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTGCCAGCAGCAGCGG 16
Db      161 GTGCCAGCAGCAGCGG 176
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RESULT 11
PCT-US04-05092-48
; Sequence 48, Application PC/TUS0405092
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; RAMKUMAR, Jayalaxmi;
; APPLICANT: MARQUIS, Joseph P.; SWARNAKAR, Anita;
; APPLICANT: CHAWLA, Narinder K.; TRAN, Uyen K.;
; APPLICANT: BECHA, Shanya; LEE, Soo Yeun;
; APPLICANT: HAFALIA, April J.A.; RICHARDSON, Thomas;
; APPLICANT: KHARE, Reena; JIANG, Xin;
; APPLICANT: JACKSON, Alan; YANG, Junming;
; APPLICANT: GORVAD, Ann
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PF-1643 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/05092
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US 60/449,059
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/456,932
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: US 60/458,844
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/461,678
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/463,937
; PRIOR FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523794CB1
PCT-US04-05092-48
Query Match 76.2%; Score 16; DB 1; Length 1647;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGCAGCAGCGGTAA 19
DB 856 CCAGCAGCAGCGGTAA 871

RESULT 12
US-10-767-471-10719/c
; Sequence 10719, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10719
; LENGTH: 109725
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-10719
Query Match 76.2%; Score 16; DB 7; Length 109725;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGCAGCAGCGGTAA 21
DB 26803 AGCAGCAGCGGTAA 26788

RESULT 13
US-10-425-115-139088/c
; Sequence 139088, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: KOVALLIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 139088
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_58330C.1
US-10-425-115-139088
Query Match 71.4%; Score 15; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCG 15
DB 138 GTGCCAGCAGCAGCG 124

RESULT 14
PCT-US04-12047-347/c
; Sequence 347, Application PC/TUS0412047
; GENERAL INFORMATION:
; APPLICANT: FIVE PRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; FILE REFERENCE: 08940.0021-00304
; CURRENT APPLICATION NUMBER: PCT/US04/12047
; CURRENT FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 1464
; PRIOR APPLICATION NUMBER: US 60/463,732
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/463,708
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/467,230
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/467,199
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/493,573
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/493,577
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/486,480
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US 60/486,446
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US 60/471,306
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/471,336
; PRIOR FILING DATE: 2003-05-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 347
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-12047-347
Query Match 71.4%; Score 15; DB 1; Length 213;
Best Local Similarity 100.0%; Pred. No. 98;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCG 15
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Db 43 GTGCCAGCAGCAGCG 29

RESULT 15
US-10-425-115-49000/c
; Sequence 49000, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 49000
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144694C.1
US-10-425-115-49000

Query Match 71.4%; Score 15; DB 6; Length 260;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCG 15
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Db 160 GTGCCAGCAGCAGCG 146

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105: /cgn2_6/ptodata/2/pna/US6048 COMB.seq.*
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109: /cgn2_6/ptodata/2/pna/US6052 COMB.seq.*
110: /cgn2_6/ptodata/2/pna/US6053 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	39	US-09-940-860-4
2	21	100.0	5849	19	US-09-369-922-1
3	21	100.0	5849	19	US-09-369-922-1
4	19	90.5	108	68	US-60-128-433-3619
5	19	90.5	116	68	US-09-540-235-4801
6	19	90.5	195	68	US-60-128-433-4848
7	19	90.5	239	23	US-09-540-235-5333
8	19	90.5	282	68	US-60-128-433-3158
9	19	90.5	287	68	US-60-128-433-2909
10	19	90.5	285	23	US-09-540-235-1015
11	19	90.5	295	68	US-60-128-433-1486
12	19	90.5	300	23	US-09-540-235-4526
13	19	90.5	301	23	US-09-540-235-3580
14	19	90.5	301	68	US-60-128-433-5580
15	19	90.5	302	23	US-09-540-235-4559
16	19	90.5	335	23	US-09-540-235-2070
17	19	90.5	335	68	US-60-128-433-3019
18	19	90.5	343	23	US-09-540-235-1051
19	19	90.5	343	68	US-60-128-433-1529
20	19	90.5	351	23	US-09-540-235-3693
21	19	90.5	357	68	US-60-128-433-2469
22	19	90.5	358	23	US-09-540-235-3256
23	19	90.5	358	68	US-60-128-433-5014
24	19	90.5	362	68	US-60-128-433-849
25	19	90.5	364	23	US-09-540-235-2614
26	19	90.5	364	68	US-60-128-433-3929
27	19	90.5	370	68	US-60-128-433-3517
28	19	90.5	371	68	US-60-128-433-666
29	19	90.5	372	23	US-09-540-235-3216
30	19	90.5	372	68	US-60-128-433-4850
31	19	90.5	375	23	US-09-540-235-2809
32	19	90.5	375	68	US-60-128-433-3924
33	19	90.5	379	23	US-09-540-235-3911
34	19	90.5	380	23	US-09-540-235-4757
35	19	90.5	384	68	US-60-128-433-4162
36	19	90.5	385	23	US-09-540-235-453
37	19	90.5	385	68	US-60-128-433-679
38	19	90.5	386	68	US-60-128-433-913
39	19	90.5	387	68	US-60-128-433-1726
40	19	90.5	389	23	US-09-540-235-2103
41	19	90.5	389	68	US-60-128-433-3100
42	19	90.5	390	23	US-09-540-235-4142
43	19	90.5	394	23	US-09-540-235-3185
44	19	90.5	394	68	US-60-128-433-4897
45	19	90.5	395	23	US-09-540-235-1153

ALIGNMENTS

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RESULT 1
US-09-940-860-4
; Sequence 4, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940, 860
; CURRENT FILING DATE: 2001-08-29
; PRIOR FILING DATE: 2000-08-31
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-4
Query Match 100.0%; Score 21; DB 39; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCCAGCAGCAGCGGTAATA 21
Db 1 GTGCCAGCAGCAGCGGTAATA 21
RESULT 2
US-09-369-922-1
; Sequence 1, Application US/09369922
; GENERAL INFORMATION:
; APPLICANT: Kara, Anna K.
; APPLICANT: Ting, Robert C.
; APPLICANT: Tam, Jill M.
; APPLICANT: Nelson, James S.
; APPLICANT: Tan, Theresa M.
; TITLE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of
; FILE OF INVENTION: Extrachromosomal Genetic Material
; FILE REFERENCE: 64-99
; CURRENT APPLICATION NUMBER: US/09/369,922
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/IB98/00212
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: AU P09481/97
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: AU P09329/97
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: AU P04953/97
; PRIOR FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5849
; TYPE: DNA
; ORGANISM: Plasmodium berghei
US-09-369-922-1
Query Match 100.0%; Score 21; DB 19; Length 5849;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCCAGCAGCAGCGGTAATA 21
Db 4671 GTGCCAGCAGCAGCGGTAATA 4691
RESULT 3
US-09-369-922C-1
; Sequence 1, Application US/09369992C
; GENERAL INFORMATION:
; APPLICANT: Kara, Anna K.
; APPLICANT: Ting, Robert C.
; APPLICANT: Tam, Jill M.
; APPLICANT: Nelson, James S.
; APPLICANT: Tan, Theresa M.
; TITLE OF INVENTION: Diagnosis of Parasites
; FILE REFERENCE: 64-99
; CURRENT APPLICATION NUMBER: US/09/369,992C
; CURRENT FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/IB98/00212
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: AU P09481/97
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: AU P09329/97
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: AU P04953/97
; PRIOR FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 53

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5849
; TYPE: DNA
; ORGANISM: Plasmodium berghei
US-09-369-992C-1

Query Match      100.0%; Score 21; DB 19; Length 5849;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 21
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Db 4671 GTGCCAGCAGCAGCGGTAA 4691

RESULT 4
US-60-128-439-3619
; Sequence 3619, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalguadi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 3619
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
US-60-128-439-3619

Query Match      90.5%; Score 19; DB 68; Length 108;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
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Db 88 GTGCCAGCAGCAGCGGTAA 106

RESULT 5
US-09-540-235-4801
; Sequence 4801, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalguadi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4801
; LENGTH: 116
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
US-09-540-235-4801

Query Match      90.5%; Score 19; DB 23; Length 116;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
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Db 96 GTGCCAGCAGCAGCGGTAA 114
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RESULT 6
US-60-128-439-4848
; Sequence 4848, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalguadi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 4848
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-60-128-439-4848

Query Match      90.5%; Score 19; DB 68; Length 195;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
    |||||
Db 114 GTGCCAGCAGCAGCGGTAA 132

RESULT 7
US-09-540-235-5333
; Sequence 5333, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalguadi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5333
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-09-540-235-5333

Query Match      90.5%; Score 19; DB 23; Length 239;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
    |||||
Db 154 GTGCCAGCAGCAGCGGTAA 172

RESULT 8
US-60-128-439-3158
; Sequence 3158, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalguadi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
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; SEQ ID NO 3158
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-60-128-439-3158

Query Match 90.5%; Score 19; DB 69; Length 282;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
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DB 51 GTGCCAGCAGCAGCGGTAA 69
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RESULT 9
US-60-128-439-2909
; Sequence 2909, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 2909
; LENGTH: 287
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11
US-60-128-439-2909

Query Match 90.5%; Score 19; DB 68; Length 287;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
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DB 56 GTGCCAGCAGCAGCGGTAA 74
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RESULT 10
US-09-540-235-1015
; Sequence 1015, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1015
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-09-540-235-1015

Query Match 90.5%; Score 19; DB 23; Length 295;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||||

DB 137 GTGCCAGCAGCAGCGTAA 155
RESULT 11
US-60-128-439-1486
; Sequence 1486, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 1486
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-60-128-439-1486

Query Match 90.5%; Score 19; DB 68; Length 295;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||||
DB 137 GTGCCAGCAGCAGCGGTAA 155
|||||

RESULT 12
US-09-540-235-4526
; Sequence 4526, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4526
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11
US-09-540-235-4526

Query Match 90.5%; Score 19; DB 23; Length 300;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||||
DB 56 GTGCCAGCAGCAGCGGTAA 74
|||||

RESULT 13
US-09-540-235-3580
; Sequence 3580, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3580
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-09-540-235-3580

Query Match 90.5%; Score 19; DB 23; Length 295;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||||

; CURRENT FILING DATE: 2000-04-03 60/128,439
; PRIOR APPLICATION NUMBER: 1999-04-06
; PRIOR FILING DATE: 1999-04-06 5674
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3580
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6
US-09-540-235-3580

Query Match 90.5%; Score 19; DB 23; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||
Db 160 GTGCCAGCAGCAGCGGTAA 178

RESULT 14
US-60-128-439-5580
; Sequence 5580, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 5580
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6
US-60-128-439-5580

Query Match 90.5%; Score 19; DB 68; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||
Db 160 GTGCCAGCAGCAGCGGTAA 178

RESULT 15
US-09-540-235-4659
; Sequence 4659, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4659
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-09-540-235-4659

Query Match 90.5%; Score 19; DB 23; Length 302;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGGTAA 19
|||
Db 71 GTGCCAGCAGCAGCGGTAA 89

Search completed: August 4, 2004, 11:29:59
Job time : 1918.07 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 37.9518 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-4

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

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- 5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	76.2	426	US-09-252-991A-7151	Sequence 7151, Ap
2	16	76.2	684	US-09-328-352-2320	Sequence 2320, Ap
3	16	76.2	783	US-09-252-991A-7428	Sequence 7428, Ap
4	16	76.2	2841	US-09-252-991A-7209	Sequence 7209, Ap
5	16	76.2	3099	US-09-252-991A-7487	Sequence 7487, Ap
6	15	71.4	32	US-09-807-784B-11	Sequence 11, Appl
7	15	71.4	387	US-09-540-236-1498	Sequence 1498, Ap
8	15	71.4	398	US-09-621-976-9153	Sequence 9153, Ap
9	15	71.4	558	US-09-540-236-958	Sequence 958, App
10	15	71.4	828	US-09-489-039A-4976	Sequence 4976, Ap
11	15	71.4	1050	US-09-252-991A-1269	Sequence 1269, Ap
12	15	71.4	1308	US-09-252-991A-1179	Sequence 1179, Ap
13	15	71.4	1575	US-08-639-294-1	Sequence 1, Appl
14	15	71.4	1575	US-09-861-034B-1	Sequence 1, Appl
15	15	71.4	1915	US-09-147-915-1	Sequence 1, Appl
16	15	71.4	2186	US-09-184-001-1	Sequence 1, Appl
17	15	71.4	2558	US-09-184-001-3	Sequence 3, Appl
18	15	71.4	3762	US-09-489-039A-4926	Sequence 4926, Ap
19	15	71.4	62903	US-09-596-002-32	Sequence 32, Appl
20	15	71.4	269223	US-09-596-002-41	Sequence 41, Appl
21	15	71.4	4403765	US-09-103-840A-2	Sequence 2, Appl
22	15	71.4	4411529	US-09-103-840A-2	Sequence 1, Appl
23	14	66.7	15	US-09-275-850-25	Sequence 25, Appl
24	14	66.7	17	US-08-554-612C-35	Sequence 35, Appl
25	14	66.7	39	US-08-721-458B-67	Sequence 67, Appl
26	14	66.7	41	US-08-721-458B-68	Sequence 68, Appl
27	14	66.7	69	US-08-554-612C-37	Sequence 37, Appl

C 28	14	66.7	96	4	US-09-230-233A-4	Sequence 4, Appl
C 29	14	66.7	145	1	US-08-554-612C-48	Sequence 48, Appl
C 30	14	66.7	225	4	US-09-621-976-538	Sequence 538, App
C 31	14	66.7	357	4	US-09-489-039A-909	Sequence 909, App
C 32	14	66.7	360	4	US-09-107-532A-181	Sequence 181, App
C 33	14	66.7	407	4	US-09-621-976-3580	Sequence 3580, Ap
C 34	14	66.7	423	4	US-09-252-991A-606	Sequence 606, App
C 35	14	66.7	423	4	US-09-252-991A-9188	Sequence 9188, Ap
C 36	14	66.7	423	4	US-09-252-991A-9323	Sequence 9323, Ap
C 37	14	66.7	426	4	US-09-252-991A-14686	Sequence 14686, A
C 38	14	66.7	429	4	US-09-252-991A-6653	Sequence 6653, Ap
C 39	14	66.7	459	4	US-09-621-976-3656	Sequence 3656, Ap
C 40	14	66.7	471	4	US-09-252-991A-10011	Sequence 10011, A
C 41	14	66.7	471	4	US-09-489-039A-269	Sequence 269, App
C 42	14	66.7	471	4	US-09-489-039A-1151	Sequence 1151, Ap
C 43	14	66.7	483	1	US-08-554-612C-15	Sequence 15, Appl
C 44	14	66.7	495	4	US-09-252-991A-15946	Sequence 15946, A
C 45	14	66.7	540	4	US-09-489-039A-156	Sequence 156, App

ALIGNMENTS

RESULT 1
US-09-252-991A-7151
; Sequence 7151, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7151
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (256)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7151

Query Match 75.2%; Score 16; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCGCGG 16
Db 46 GTGCCAGCAGCGCGG 61

RESULT 2
US-09-328-352-2320
; Sequence 2320, Application US/09328352
; Patent No. 4562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2320
; LENGTH: 684
; TYPE: DNA

; ORGANISM: Acinetobacter baumannii
US-09-328-352-2320

Query Match 76.2%; Score 16; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAGCAGCAGCGGTAAT 20
|||||
DB 170 CAGCAGCAGCGGTAAT 185

RESULT 3

US-09-252-991A-7428/c
; Sequence 7428, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7428
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: unsure
; LOCATION: (422)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7428

Query Match 76.2%; Score 16; DB 4; Length 783;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
|||||
DB 632 GTGCCAGCAGCAGCGG 617

RESULT 4

US-09-252-991A-7209
; Sequence 7209, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7209
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: unsure
; LOCATION: (2058)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7209

Query Match 76.2%; Score 16; DB 4; Length 2541;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
|||||
DB 1848 GTGCCAGCAGCAGCGG 1863

RESULT 5

US-09-252-991A-7487/c
; Sequence 7487, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7487
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: unsure
; LOCATION: (1117)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7487

Query Match 76.2%; Score 16; DB 4; Length 3099;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCGG 16
|||||
DB 1327 GTGCCAGCAGCAGCGG 1312

RESULT 6

US-09-807-784B-11/c
; Sequence 11, Application US/09807784B
; Patent No. 6653118
; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; APPLICANT: Shikawa, Daisuke
; TITLE OF INVENTION: No. 6653118el Deoxyribonuclease, Gene Encoding Thereof and Use Th
; FILE REFERENCE: 210792
; CURRENT APPLICATION NUMBER: US/09/807,784B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: JP 11-230870
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 11
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide designed to act as sense primer for
; OTHER INFORMATION: amplifying coding sequence of DNaase II signal peptide.
US-09-807-784B-11

Query Match 71.4%; Score 15; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCAGCAGCGG 16
|||||

Db 32 TGCCAGCAGCAGCGG 18

RESULT 7

US-09-540-236-1498/c
; Sequence 1498, Application US/09540236
; Patent No. 6673910

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 1498

; LENGTH: 387

; TYPE: DNA

; ORGANISM: M.catarrhalis

US-09-540-236-1498

Query Match 71.4%; Score 15; DB 4; Length 387;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCAGCAGCGG 16

|||||

Db 274 TGCCAGCAGCAGCGG 260

RESULT 8

US-09-621-976-9153/c
; Sequence 9153, Application US/09621976
; Patent No. 6639063

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 9153

; LENGTH: 398

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 320

; OTHER INFORMATION: n=a, g, c or t

US-09-621-976-9153

Query Match 71.4%; Score 15; DB 4; Length 398;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCAGCAGCGG 16

|||||

Db 126 TGCCAGCAGCAGCGG 112

RESULT 9

US-09-540-236-958/c
; Sequence 958, Application US/09540236
; Patent No. 6673910

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

US-09-540-236-958

; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 958

; LENGTH: 558

; TYPE: DNA

; ORGANISM: M.catarrhalis

US-09-540-236-958

Query Match 71.4%; Score 15; DB 4; Length 558;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AGCAGCAGCGGTAAT 20

|||||

Db 231 AGCAGCAGCGGTAAT 217

RESULT 10

US-09-489-039A-4976

; Sequence 4976, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 4976

; LENGTH: 828

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4976

Query Match 71.4%; Score 15; DB 4; Length 828;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCAGCAGCGG 16

|||||

Db 432 TGCCAGCAGCAGCGG 446

RESULT 11

US-09-252-991A-1269/c

; Sequence 1269, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1269

; LENGTH: 1050

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1269

Query Match 71.4%; Score 15; DB 4; Length 1050;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAGCAGCAGCGGTA 18

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Db      818 CCAGCAGCAGCGGTA 804
|||||
RESULT 12
US-09-252-991A-1179/c
; Sequence 1179, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1179
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1179

Query Match      71.4%; Score 15; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CCAGCAGCAGCGGTA 18
|||||
Db      868 CCAGCAGCAGCGGTA 854

RESULT 13
US-08-639-294-1/c
; Sequence 1, Application US/08639294
; Patent No. 6265195
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Human DNase II
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION NUMBER: US/08/639,294
; FILING DATE: 25-Apr-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3562
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1575 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single

Db      818 CCAGCAGCAGCGGTA 804
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RESULT 14
US-09-861-034B-1/c
; Sequence 1, Application US/09861034B
; Patent No. 6569429
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Human DNase II
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION NUMBER: US/09/861,034B
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639294
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1024D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1575 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-034B-1

Query Match      71.4%; Score 15; DB 4; Length 1575;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TCCAGCAGCAGCGG 16
|||||
Db      106 TCCAGCAGCAGCGG 92
|||||

RESULT 15
US-09-147-915-1/c
; Sequence 1, Application US/09147915A
; Patent No. 6184034
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan
```

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; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
US-08-639-294-1

Query Match      71.4%; Score 15; DB 3; Length 1575;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TCCAGCAGCAGCGG 16
|||||
Db      106 TCCAGCAGCAGCGG 92
|||||

RESULT 14
US-09-861-034B-1/c
; Sequence 1, Application US/09861034B
; Patent No. 6569429
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Human DNase II
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION NUMBER: US/09/861,034B
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/639294
; FILING DATE: 25-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1024D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1575 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-034B-1

Query Match      71.4%; Score 15; DB 4; Length 1575;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TCCAGCAGCAGCGG 16
|||||
Db      106 TCCAGCAGCAGCGG 92
|||||

RESULT 15
US-09-147-915-1/c
; Sequence 1, Application US/09147915A
; Patent No. 6184034
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan
```



```

; APPLICANT: Krieser, Ronald
; TITLE OF INVENTION: Deoxyribonuclease II Proteins and cDNAs
; FILE REFERENCE: DC-0097
; CURRENT APPLICATION NUMBER: US/09/147,915A
; CURRENT FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: PCT/US97/18262
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/028,539
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-147-915-1

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Query Match      71.4%; Score 15; DB 3; Length 1915;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  TGCCAGCAGCGG 16
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Db      88  TGCCAGCAGCGG 74

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 Job time : 42.9518 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1532.58 Seconds
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Title: US-09-940-860-3

Perfect score: 22

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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vri:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	16	72.7	258	10 BF064383	BF064383 SWOVAFCAP
C 3	16	72.7	262	9 AI585049	AI585049 fb69g07.x
C 4	16	72.7	285	9 AI211182	AI211182 c0c05a1.f

C 5	16	72.7	324	9 AI381122	AI381122 SWOVAFCAP
C 6	16	72.7	348	9 AA497171	AA497171 fa01g09.s
C 7	16	72.7	367	12 BI897005	BI897005 fk52e10.y
C 8	16	72.7	371	12 BI897004	BI897004 fk52e10.x
C 9	16	72.7	377	9 AA784579	AA784579 flh09a1.f
C 10	16	72.7	445	12 BI896339	BI896339 fc43d02.x
C 11	16	72.7	445	12 BI896339	BI896339 fv18f06.y
C 12	16	72.7	448	12 BI533213	BI533213 f-79a06.x
C 13	16	72.7	452	12 BM102203	BM102203 fv14d10.x
C 14	16	72.7	458	12 BI896999	BI896999 fk50e03.x
C 15	16	72.7	459	12 BI708149	BI708149 fs42g04.x
C 16	16	72.7	466	12 BI866073	BI866073 ft98a01.x
C 17	16	72.7	471	12 BM102107	BM102107 fv13a06.x
C 18	16	72.7	477	9 AI087773	AI087773 SWOVAFCAP
C 19	16	72.7	478	14 CB081772	CB081772 bk56g09.g
C 20	16	72.7	491	12 BI472977	BI472977 ff94c06.y
C 21	16	72.7	496	10 AW281793	AW281793 fj56h02.x
C 22	16	72.7	530	12 BI708185	BI708185 fs43c07.x
C 23	16	72.7	543	12 BI981155	BI981155 fu40d12.x
C 24	16	72.7	544	10 AW179661	AW179661 SWYD25CAU
C 25	16	72.7	545	9 AI353986	AI353986 zeh1247.s
C 26	16	72.7	568	9 AW077500	AW077500 fj35a03.y
C 27	16	72.7	569	12 BM024042	BM024042 fu69a03.y
C 28	16	72.7	591	12 BM070610	BM070610 fv02b01.y
C 29	16	72.7	622	14 CD014811	CD014811 hac25b10.
C 30	16	72.7	672	12 BP176156	BP176156 BP176156
C 31	16	72.7	679	12 BP176155	BP176155 BP176155
C 32	16	72.7	692	13 BU006325	BU006325 QGH10109.
C 33	16	72.7	702	14 CB678345	CB678345 OSNBE16D
C 34	16	72.7	759	28 BZ066995	BZ066995 lj1c3g07.
C 35	16	72.7	768	28 BZ067045	BZ067045 lj1c3g07.
C 36	15	68.2	275	14 CD857812	CD857812 DHOAGS2C0
C 37	15	68.2	295	14 CD856759	CD856759 DHOAG23ZD
C 38	15	68.2	304	14 CD857406	CD857406 DHOAG19ZD
C 39	15	68.2	313	14 CD857943	CD857943 DHOAG6ZF0
C 40	15	68.2	319	14 CD858282	CD858282 DHOAG14ZE
C 41	15	68.2	326	14 CD856671	CD856671 DHOAG22ZD
C 42	15	68.2	326	14 CD856685	CD856685 DHOAG22ZE
C 43	15	68.2	326	14 CD856795	CD856795 DHOAG23ZG
C 44	15	68.2	344	14 CD858273	CD858273 DHOAG14ZD
C 45	15	68.2	345	14 CD856625	CD856625 DHOAG21ZH

ALIGNMENTS

RESULT 1
AI212321/c

LOCUS
DEFINITION

AI212321 213 bp mRNA linear EST 19-OCT-1998
x2902a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
x2902a1 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI212321.1 GI:3774263
EST
Emericella nidulans (anamorph: Aspergillus nidulans)
Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 213)
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
Prade, R. and Rose, B.
An Aspergillus nidulans EST Database
Unpublished (1998)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center

Seq primer: M13-20
High quality sequence stop: 88.
Location/Qualifiers
1. .213
/organism="Emericella nidulans"
/mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="X2902a1"
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
|||||
Db 98 CCCGAGAACGTATTCA 83
|||||

RESULT 2
BF064383 258 bp mRNA linear EST 17-OCT-2000
LOCUS SNOVAFCAP49B11SK Onchocerca volvulus adult female cDNA
DEFINITION (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SNOVAFCAP49B11 5', mRNA sequence.

ACCESSION BF064383.1 GI:10841022
VERSION BF064383
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 258)
Lizotte-Waniewski, M. and Williams, S.A.
Genes expressed in adult female stage of Onchocerca volvulus
Unpublished (1998)
CONTACT: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1. .258
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SNOVAFCAP49B11"
/sex="female"
/dev_stage="adult"
/lab_host="XLI-Blue MRF"
/clone_lib="Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7 x 10E5 independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available

ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
|||||
Db 102 CCCGAGAACGTATTCA 87
|||||

RESULT 3
AI585049/c 262 bp mRNA linear EST 07-JUN-2001
LOCUS f69g07.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
DEFINITION IMAGE:3717180 3', mRNA sequence.

ACCESSION AI585049
VERSION AI585049.1 GI:4570946
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 262)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
CONTACT: Stephen L. Johnson
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center. Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and Ressourcenzentrum Primardatenbank, Berlin, Germany (web address: www.rzpd.de)
Zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 ET from Amersham
High quality sequence stop: 254
POLYA=No.

FEATURES
source
1. .262
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3717180"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield stage embryos"
/lab_host="XLI-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTCTAGCCGAGCCGCCCTTTTCTTTTCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST

from Dr. Steven A. Williams, email: genome@smith.edu."

analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCGAGACGTA 18
|||||

Db 196 AAGGCCGAGACGTA 181

RESULT 4

AI211182/c 285 bp mRNA linear EST 19-OCT-1998
LOCUS oco05al.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
oco05al 3', mRNA sequence.

ACCESSION

AI211182 GI:3773124

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Emericella nidulans (anamorph: Aspergillus nidulans)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; Emericella.

REFERENCE

1. (bases 1 to 285)

AUTHORS

Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,

Prade, R., and Roe, B.

An Aspergillus nidulans EST Database

Other ESTs: oco05al.r1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal

Genetics Stock Center

Seq primer: M13-20

High quality sequence stop: 219.

FEATURES

source

1..285

/organism="Emericella nidulans"

/mol_type="mRNA"

/strain="FGSC A26"

/db_xref="taxon:162425"

/clone="oco05al"

/tissue_type="vegetative mycelia, asexual structures"

/clone_lib="Aspergillus nidulans 24hr asexual

developmental and vegetative cDNA lambda zap library"

/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

3' end of cDNA cloned into XhoI site of pBluescript"

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCCGAGACGTATTC A 22
|||||

Db 92 CCCGAGACGTATTC A 77

RESULT 5

AI381122/c

LOCUS

DEFINITION

AI381122

AI381122.1

AI381122

AI381122.1

AI381122.1

AI381122.1

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AI381122.1

AI381122.1

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 348)

AUTHORS Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE WashU Zebrafish EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Steve Johnson lab internal ID - P1.89 NOTE - For this library, the CLONE id field represents a position identifier on the original cDNA library preparation plate. cDNA Library Preparation: Matthew Clark; cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare Genetik, Berlin Tel +49 30 84 13 1235
Seq primer: -40m13 ET from Amersham
High quality sequence stop: 315.

FEATURES

source 1..348
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="3D9"
/sex="mixed"
/tissue types="pooled 26-somite embryos"
/lab host="X1-blue MRP"
/clone lib="Zebrafish ICRFzfls"
/notes="vector: pSPORT1, Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo (GT)15 primer [5'pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT3'], on mRNA from pooled 26 somite zebrafish embryos; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin) and was not biochemically normalised. 70,000 clones from this library were arrayed on high density filters and subsequently screened by oligonucleotide hybridization fingerprinting to identify unique or minimally redundant clones for more intensive analysis."

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGCGCCGAGACGTA 18
|||||

Db 196 AAGCGCCGAGACGTA 181
|||||

RESULT 7

LOCUS BI897005

DEFINITION fK52e10.y1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 5', mRNA sequence.

ACCESSION BI897005

VERSION BI897005.1 GI:16140141

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 367)

AUTHORS Clark, M., Johnson, S., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE WashU Zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine

AUTHORS Clark, M., Johnson, S., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE WashU Zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine

FEATURES

source 1..367
/organism="Danio rerio"
/mol_type="mRNA"
/strain="unspecified"
/db_xref="taxon:7955"
/sex="mixed"
/dev stage="15-19 hour embryo"
/lab host="E.Coli (DH10B/XL2blue)"
/clone lib="Zebrafish 15-19hr embryonic cDNA"
/notes="vector: pSPORT1; Site 1: NotI; Site 2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@kfz-heidelberg.de). RZPD library number: 717"

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 367;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGCGCCGAGACGTA 18
|||||

Db 250 AAGCGCCGAGACGTA 265
|||||

RESULT 8

LOCUS BI897004/c

DEFINITION fK52e10.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3', mRNA sequence.

ACCESSION BI897004

VERSION BI897004.1 GI:16140140

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 371)

AUTHORS Clark, M., Johnson, S., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE WashU Zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine

double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCCGAGACGTA 18
|||||
DB 189 AAGGCCCGAGACGTA 174

RESULT 11

BM156391/c
LOCUS BM156391 445 bp mRNA linear EST 26-JUL-2002
DEFINITION fvl8f06.y2 zebrafish adult brain Danio rerio cDNA clone
IMAGE:5386907 5', mRNA sequence.
ACCESSION BM156391
VERSION BM156391.1 GI:17240087
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Other ESTs: fvl8f06.x2

TITLE

WashU Zebrafish EST Project 1998
JOURNAL
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrfish@watson.wustl.edu

cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

Putative full length read

The vector to vector length is 522

Seq primer: T7.

FEATURES

source
1. .445
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5386907"
/sex="mixed male and female"

/tissue_type="brain"
/dev_stage="adult"

/lab_host="E. coli DH10B"

/clone_lib="zebrafish adult brain"

/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCCGAGACGTA 18
|||||
DB 16 AAGGCCCGAGACGTA 1

RESULT 12

BI533213/c
LOCUS BI533213 448 bp mRNA linear EST 26-JUL-2002
DEFINITION fr79a06.x1 zebrafish adult brain Danio rerio cDNA clone
IMAGE:4966930 3', mRNA sequence.
ACCESSION BI533213
VERSION BI533213.1 GI:15373780
KEYWORDS EST.

SOURCE

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

TITLE

WashU Zebrafish EST Project 1998

JOURNAL

COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbrfish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: -40UP
High quality sequence stop: 408.
Location/Qualifiers
1. .448
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4966930"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;

FEATURES

source
1. .448
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4966930"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;

Original library was constructed in lambdaZIPLOX. Mass
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 448;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCCGAGAACGTA 18
|||||
Db 181 AAGGCCCGAGAACGTA 166
|||||

RESULT 13

BM102203/c
LOCUS 452 bp mRNA linear EST 26-JUL-2002
DEFINITION fvi4d10.x1 zebrafish adult brain Danio rerio cDNA clone
IMAGE:5386435 3', mRNA sequence.

ACCESSION BM102203
VERSION BM102203.1 GI:17033271

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 452)

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

TITLE

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center Clone Distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:

gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio

rerio cDNA

Seq primer: -40UP

High quality sequence stop: 451.

Location/Qualifiers

1..452

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:5386435"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

/lab_host="E. coli DH10B"

/clone_lib="zebrafish adult brain"

/notes="Vector: pZIPLOX; Site 1: NotI; Site 2: SalI;

Original library was constructed in lambdaZIPLOX. Mass

excision of the cDNA library was performed to yield

pZIPLOX plasmids. Insert check was done in original

library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 452;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCCGAGAACGTA 18

|||||

Db 180 AAGGCCCGAGAACGTA 165

|||||

RESULT 14

BI896999/c

LOCUS 458 bp mRNA linear EST 15-OCT-2001

DEFINITION fk50e03.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3',

mRNA sequence.

ACCESSION BI896999

VERSION BI896999.1 GI:16140135

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 458)

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Other ESTs: fk50e03.y1

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

Library constructed by: Bernhard Korn DNA Sequencing by: Washington

University Genome Sequencing Center Clone Distribution:

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:

gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio

rerio cDNA

Seq primer: T7 from Gibco

High quality sequence stop: 434.

Location/Qualifiers

1..458

/organism="Danio rerio"

/mol_type="mRNA"

/strain="unspecified"

/db_xref="taxon:7955"

/sex="mixed"

/dev_stage="15-19 hour embryo"

/lab_host="E. coli (DH10B/XL2blue)"

/clone_lib="Zebrafish 15-19hr embryonic cDNA"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This

zebrafish library was constructed by Dr. Bernhard Korn

(email: b.korn@dkfz-heidelberg.de). RZPD library number:

717"

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGGCCCGAGAACGTA 18

|||||

Db 93 AAGGCCCGAGAACGTA 78

|||||

```

RESULT 15
BI708149/c
LOCUS      BI708149          459 bp      mRNA      linear      EST 19-SEP-2001
DEFINITION f542g04.x1 Zebrafish adult olfactory Danio rerio cDNA clone
IMAGE:5070534 3', mRNA sequence.
ACCESSION  BI708149
VERSION     BI708149.1  GI:15683844
KEYWORDS   EST
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 459)
AUTHORS     Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
            Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, F.,
            Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
            Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
            Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
            Waterston, R. and Wilson, R.
            WashU Zebrafish EST Project 1998
            Unpublished (1998)
OTHER_SEQS  f542g04.y1
CONTACT     Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrfish@watson.wustl.edu
ENAIL: zbrfish@watson.wustl.edu
CMAIL Library Preparation: John Ngai cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimaDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to:
gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRPzfls Danio
rerio cDNA
Seq primer: T7 from Gibco
High quality sequence stop: 440.
FEATURES
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    1..459
        /organism="Danio rerio"
        /mol_type="mRNA"
        /db_xref="taxon:7955"
        /clone="IMAGE:5070534"
        /sex="mixed"
        /tissue_type="Olfactory rosettes"
        /dev_stage="adult"
        /lab_host="D10Hb (Gibco BRL)"
        /clone_lib="Zebrafish adult olfactory"
        /notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This
            is a directionally cloned cDNA library from adult
            Zebrafish olfactory epithelium."
ORIGIN
Query Match      72.7%; Score 16; DB 12; Length 459;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  AAGGCCCGAGACGTA 18
      |||||
DB      167 AAGGCCCGAGACGTA 152

Search completed: August 4, 2004, 09:20:54
Job time : 1535.58 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 164.337 Seconds

(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggagggaagcgaggatgacg 20

Scoring table:

OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	1172	3	AAA37798 Helicobac
2	20	100.0	1194	3	AAA37797 Helicobac
3	20	100.0	1236	3	AAA37796 Helicobac
4	20	100.0	1267	3	AAA37795 Helicobac
5	20	100.0	1299	3	AAA37794 Helicobac
6	20	100.0	1331	3	AAA37793 Helicobac
7	20	100.0	1335	3	AAA37791 Helicobac
8	20	100.0	1548	2	AAV66849 Chlamydia
9	20	100.0	1548	2	AAV66846 Chlamydia
10	20	100.0	1548	2	AAV66848 Chlamydia
11	20	100.0	1548	2	AAV66845 Chlamydia
12	20	100.0	1548	2	AAV66850 Chlamydia
13	20	100.0	1548	2	AAV66847 Chlamydia
14	20	100.0	1548	5	AAV66847 Chlamydia
15	20	100.0	1549	2	AAV66851 Chlamydia
16	20	100.0	2751	4	AAH28376 Intergeri
17	20	100.0	2762	4	AAH28407 Intergeri
18	20	100.0	110000	2	AAH28407 Intergeri
19	20	100.0	110000	2	AAH28407 Intergeri
20	17	85.0	1073	7	AB234585 Coding se
21	16	80.0	1251	7	ACA30087 Prokaryot
22	16	80.0	3264	7	ADA69779 Rice gene
23	16	80.0	5536	4	AAS46575 Tumour su

ALIGNMENTS

RESULT 1

AAA37798

ID AAA37798 standard; DNA; 1172 BP.

XX AAA37798;

AC AAA37798;

DT 15-SEP-2003 (revised)

DT 15-JAN-2001 (first entry)

XX Helicobacter 16S rRNA DNA sequence R28TOTALL.

XX Helicobacter; 16S rRNA; detection; strain identification; gastric ulcer;

KW chronic gastritis; zoonoses; ss.

XX Candidatus Helicobacter bovis.

OS

PN EPI035219-A1.

XX 13-SEP-2000.

XX 25-FEB-1999; 99EP-00870035.

XX 25-FEB-1999; 99EP-00870035.

PR (UYGE-) UNIV GENT.

XX Ducatelle R, De Grootte D, Haesebrouck F, Quint W, Van Doorn L;

WPI; 2000-559879/52.

PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or

PT primers for detecting and/or typing Helicobacter strains present in a

XX biological sample.

XX Claim 2; Page 24-25; 132pp; English.

XX This sequence represents a Helicobacter 16S rRNA sequence of the

CC invention. A probe which specifically hybridises to the 16S rRNA sequence

CC and a primer which specifically amplifies it are used for detecting

CC and/or typing Helicobacter strains present in a biological sample

CC (obtained from mammals preferably cattle and pigs) by hybridising or

CC specifically amplifying the 16S rRNA gene target region of Helicobacter

CC strains present in the biological sample with the primer or probe,

CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S

CC rRNA sequences are used for studying and detecting pathogenic

CC Helicobacter strains which cause gastric ulcers and chronic gastritis in

ABL33832 Human imm
Abq78796 Nucleotid
Ab171499 Corn tass
Ab174470 Corn tass
Abq78794 Nucleotid
Aal28889 Human bre
Abq78795 Nucleotid
Abq85719 Arabidops
Aal19054 Human bre
Aal08144 Human bre
Aas79337 DNA encod
Aaf67474 Novel hum
Aaf67301 Novel hum
Abv13787 Human pro
Ab181917 Human ova
Aav89330 EST clone
Abv34900 Human pro
Abv43749 Human pro
Adc76303 DNA homol
Adc76983 DNA homol
Abz14572 Arabidops
Aac48695 Arabidops

CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)

XX Sequence 1172 BP; 323 A; 259 C; 345 G; 245 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 3; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 1 GGAGGAAGCGGAGGATGACG 20
|||||
DB 1016 GGAGGAAGCGGAGGATGACG 1035

RESULT 2
AAA37797
ID AAA37797 standard; DNA; 1194 BP.
XX
AC AAA37797;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRNA DNA sequence R27TOTAL.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EPI035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
XX WPI; 2000-559879/52.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
XX WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 2; Page 24; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)

XX Sequence 1194 BP; 327 A; 263 C; 356 G; 248 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 3; Length 1194;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 1 GGAGGAAGCGGAGGATGACG 20
|||||
DB 1016 GGAGGAAGCGGAGGATGACG 1035

DB 1035 GGAGGAAGCGGAGGATGACG 1054

RESULT 3
AAA37796
ID AAA37796 standard; DNA; 1236 BP.
XX
AC AAA37796;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRNA DNA sequence RI3D001INV.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EPI035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
XX WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 2; Page 23-24; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)

XX Sequence 1236 BP; 336 A; 271 C; 369 G; 259 T; 0 U; 1 Other;
SQ Query Match 100.0%; Score 20; DB 3; Length 1236;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 1 GGAGGAAGCGGAGGATGACG 20
|||||
DB 1058 GGAGGAAGCGGAGGATGACG 1077

RESULT 4
AAA37795
ID AAA37795 standard; DNA; 1267 BP.
XX
AC AAA37795;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX

```

DE Helicobacter 16SrRNA DNA sequence R6XA001.
XX Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX (UYGE-) UNIV GENT.
XX
XX Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX WPI; 2000-559879/52.
XX
XX Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
XX Claim 2; Page 23; 132pp; English.
XX
XX This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
XX Sequence 1267 BP; 350 A; 272 C; 375 G; 270 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 3; Length 1267;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGAAGCGGAGGATGACG 20
DB 1072 GGAGGAAGCGGAGGATGACG 1091
RESULT 5
AAA37794
ID AAA37794 standard; DNA; 1299 BP.
AC AAA37794;
XX
XX 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
XX Helicobacter 16SrRNA DNA sequence R3XA001.
DE
XX Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
XX Candidatus Helicobacter bovis.
OS
XX EP1035219-A1.
PN
XX 13-SEP-2000.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX (UYGE-) UNIV GENT.
XX
XX Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX WPI; 2000-559879/52.
XX
XX Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
XX Claim 2; Page 23; 132pp; English.
XX
XX This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
XX Sequence 1299 BP; 357 A; 283 C; 385 G; 274 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 3; Length 1299;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGAAGCGGAGGATGACG 20
DB 1103 GGAGGAAGCGGAGGATGACG 1122
RESULT 6
AAA37793
ID AAA37793 standard; DNA; 1331 BP.
AC AAA37793;
XX
XX 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
XX Helicobacter 16SrRNA DNA sequence R5XE001.
DE
XX Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
XX Candidatus Helicobacter bovis.
OS
XX EP1035219-A1.
PN
XX 13-SEP-2000.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX 25-FEB-1999; 99EP-00870035.
XX
XX (UYGE-) UNIV GENT.
XX
XX Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX WPI; 2000-559879/52.
XX
XX Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
XX Claim 2; Page 22-23; 132pp; English.
XX
XX This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
XX Sequence 1299 BP; 357 A; 283 C; 385 G; 274 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 3; Length 1299;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGAAGCGGAGGATGACG 20
DB 1103 GGAGGAAGCGGAGGATGACG 1122

```

XX Claim 2; Page 22; 132pp; English.

PS

XX This sequence represents a Helicobacter 16S rRNA sequence of the

CC invention. A probe which specifically hybridises to the 16S rRNA sequence

CC and a primer which specifically amplifies it are used for detecting

CC and/or typing Helicobacter strains present in a biological sample

CC (obtained from mammals preferably cattle and pigs) by hybridising or

CC specifically amplifying the 16S rRNA gene target region of Helicobacter

CC strains present in the biological sample with the primer or probe,

CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S

CC rRNA sequences are used for studying and detecting pathogenic

CC Helicobacter strains which cause gastric ulcers and chronic gastritis in

CC mammals, particularly cattle and pigs. The method is also useful for

CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise

CC OS field)

XX SQ Sequence 1331 BP; 366 A; 292 C; 389 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1331;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20

Db 1103 GGAGGAGGCGGAGGATGACG 1122

RESULT 7

AAA37791

ID AAA37791 standard; DNA; 1335 BP.

AC AAA37791;

XX

XX 15-SEP-2003 (revised)

DT 15-JAN-2001 (first entry)

XX

XX Helicobacter 16S rRNA DNA sequence R2XA001.

XX

XX Helicobacter; 16S rRNA; detection; strain identification; gastric ulcer;

XX chronic gastritis; zoonoses; ss.

XX

XX Candidatus Helicobacter bovis.

XX

XX EF1035219-A1.

XX

PD 13-SEP-2000.

XX

XX 25-FEB-1999; 99EP-00870035.

XX

XX 25-FEB-1999; 99EP-00870035.

XX

XX (UYGE-) UNIV GENT.

XX

XX Ducatelle R. De Groote D, Haesebrouck F, Quint W, Van Doorn L;

XX

XX WPI; 2000-559879/52.

XX

XX Novel isolated 16S rRNA Helicobacter polynucleotides useful as probes or

XX primers for detecting and/or typing Helicobacter strains present in a

XX biological sample.

XX

XX Claim 1; Page 19; 132pp; English.

PS

XX This sequence represents a Helicobacter 16S rRNA sequence of the

CC invention. A probe which specifically hybridises to the 16S rRNA sequence

CC and a primer which specifically amplifies it are used for detecting

CC and/or typing Helicobacter strains present in a biological sample

CC (obtained from mammals preferably cattle and pigs) by hybridising or

CC specifically amplifying the 16S rRNA gene target region of Helicobacter

CC strains present in the biological sample with the primer or probe,

CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S

CC rRNA sequences are used for studying and detecting pathogenic

CC Helicobacter strains which cause gastric ulcers and chronic gastritis in

CC mammals, particularly cattle and pigs. The method is also useful for

CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise

CC OS field)

XX SQ Sequence 1335 BP; 364 A; 294 C; 393 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1335;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20

Db 1103 GGAGGAGGCGGAGGATGACG 1122

RESULT 8

AAV66849

ID AAV66849 standard; DNA; 1548 BP.

XX

XX AAV66849;

XX

XX 17-OCT-2003 (revised)

DT 06-JAN-1999 (first entry)

XX

XX Chlamydia 16S ribosome RNA gene #5.

DE

XX Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.

XX

XX Chlamydothila pecorum.

XX

XX JP10262679-A.

XX

XX 06-OCT-1998.

PD

XX

XX 28-MAR-1997; 97JP-00078591.

PF

XX

XX 28-MAR-1997; 97JP-00078591.

PR

XX

XX (ATAT-) A & T KK.

PA

PA (TOKU) TOKUYAMA SODA KK.

XX

XX WPI; 1998-587294/50.

XX

XX Chlamydia species ribosome genes, and primers derived from it - used for

XX the nucleic acid amplification detection of Chlamydia species.

PT

XX

XX Claim 1; Page 15; 18pp; Japanese.

PS

XX The present sequence represents a gene coding Chlamydia 16S ribosome RNA

CC from Chlamydia pecorum. Also described in the present invention are: (1)

CC a recombinant vector containing the above gene; and (2) a transformant

CC transformed by the above recombinant vector. The nucleic acid, and

CC primers which can hybridise to it, are used for the specific nucleic acid

CC amplification detection of a Chlamydia genus microbe i.e. detection of

CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)

XX

XX SQ Sequence 1548 BP; 402 A; 318 C; 460 G; 368 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20

Db 1176 GGAGGAGGCGGAGGATGACG 1195

RESULT 9

AAV66846

ID AAV66846 standard; DNA; 1548 BP.

XX

XX AAV66846;

DR WPI; 1998-587294/50.

XX Chlamydia species ribosome genes, and primers derived from it - used for

PT the nucleic acid amplification detection of Chlamydia species.

XX

XX Claim 1; Page 14-15; 18pp; Japanese.

XX

CC The present sequence represents a gene coding Chlamydia 16S ribosome RNA

CC from Chlamydia psittaci. Also described in the present invention are: (1)

CC a recombinant vector containing the above gene; and (2) a transformant

CC transformed by the above recombinant vector. The nucleic acid, and

CC primers which can hybridise to it, are used for the specific nucleic acid

CC amplification detection of a Chlamydia genus microbe i.e. detection of

CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)

XX

XX Sequence 1548 BP; 410 A; 328 C; 452 G; 358 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 20; DB 2; Length 1548;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGCGGAGGATGACG 20

|||||

Db 1178 GGAGGAGCGGAGGATGACG 1197

RESULT 11

AAV66845

ID AAV66845 standard; DNA; 1548 BP.

XX AC AAV66845;

XX

XX 17-OCT-2003 (revised)

DT 06-JAN-1999 (first entry)

XX

XX Chlamydia 16S ribosome RNA gene #1.

XX

XX Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.

XX

XX Chlamydoiphila caviae.

XX

XX JF10262679-A.

XX

XX 06-OCT-1998.

XX

XX 28-MAR-1997; 97JP-00078591.

XX

XX 28-MAR-1997; 97JP-00078591.

PR

XX (ATAT-) A & T KK.

PA (TOKU) TOKUYAMA SODA KK.

XX

XX WPI; 1998-587294/50.

XX

XX Chlamydia species ribosome genes, and primers derived from it - used for

PT the nucleic acid amplification detection of Chlamydia species.

XX

XX Claim 1; Page 13; 18pp; Japanese.

XX

CC The present sequence represents a gene coding Chlamydia 16S ribosome RNA

CC from Chlamydia psittaci. Also described in the present invention are: (1)

CC a recombinant vector containing the above gene; and (2) a transformant

CC transformed by the above recombinant vector. The nucleic acid, and

CC primers which can hybridise to it, are used for the specific nucleic acid

CC amplification detection of a Chlamydia genus microbe i.e. detection of

CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)

XX

XX Sequence 1548 BP; 413 A; 323 C; 453 G; 359 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 20; DB 2; Length 1548;

Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGGAGGATGACG 20
 DB 1178 GGAGGAAGGCGGAGGATGACG 1197

RESULT 12
 AAV66850
 ID AAV66850 standard; DNA; 1548 BP.
 XX AC AAV66850;
 XX DT 06-JAN-1999 (first entry)
 XX DE Chlamydia 16S ribosome RNA gene #6.
 XX KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
 XX OS Chlamydia trachomatis.
 XX PN JP10262679-A.
 XX PD 06-OCT-1998.
 XX PF 28-MAR-1997; 97JP-00078591.
 XX PR 28-MAR-1997; 97JP-00078591.
 XX PA (ATAT-) A & T KK.
 XX PA (TOKU) TOKUYAMA SODA KK.
 XX DR WPI; 1998-587294/50.
 XX KW Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
 XX PS Claim 1; Page 16; 18pp; Japanese.
 XX CC The present sequence represents a gene coding Chlamydia 16S ribosome RNA from Chlamydia psittaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products.
 XX SQ Sequence 1548 BP; 402 A; 326 C; 470 G; 350 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 1548;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGGAGGATGACG 20
 DB 1179 GGAGGAAGGCGGAGGATGACG 1198

RESULT 13
 AAV66847
 ID AAV66847 standard; DNA; 1548 BP.
 XX AC AAV66847;
 XX DT 17-OCT-2003 (revised)
 XX DT 06-JAN-1999 (first entry)
 XX DE Chlamydia 16S ribosome RNA gene #3.
 XX KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
 XX OS Chlamydia caviae.
 XX PN JP10262679-A.
 XX CC

QY 1 GGAGGAAGGCGGAGGATGACG 20
 DB 1179 GGAGGAAGGCGGAGGATGACG 1198

RESULT 14
 AAS11031
 ID AAS11031 standard; DNA; 1548 BP.
 XX AC AAS11031;
 XX DT 06-AUG-2003 (revised)
 XX DT 24-OCT-2001 (first entry)
 XX DE Chlamydia trachomatis 16S ribosomal RNA gene.
 XX KW Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human; food grain supplement; livestock; poultry; therapeutic; ds.
 XX OS Chlamydia trachomatis.
 XX PN WO200142457-A2.
 XX PD 14-JUN-2001.
 XX PF 29-NOV-2000; 2000WO-US042391.
 XX PR 29-NOV-1999; 99US-0168150P.
 XX PA (AVIB-) AVI BIOPHARMA INC.
 XX PI Iversen PL;
 XX DR WPI; 2001-457295/49.
 XX PT Antibacterial compound, useful for treating bacterial infections and as livestock and poultry food supplement, comprises antisense oligonucleotides complementary to bacterial 16S and 23S rRNA.
 XX PS Disclosure; Page; 62pp; English.
 XX CC AAS11021-AAS11034 represent the coding sequences of bacterial 16S ribosomal RNA (rRNA) genes. The sequences were used to design anti-

PD 06-OCT-1998.
 XX 28-MAR-1997; 97JP-00078591.
 XX 28-MAR-1997; 97JP-00078591.
 XX (ATAT-) A & T KK.
 XX PA (TOKU) TOKUYAMA SODA KK.
 XX DR WPI; 1998-587294/50.
 XX KW Chlamydia species ribosome genes, and primers derived from it - used for the nucleic acid amplification detection of Chlamydia species.
 XX PS Claim 1; Page 14; 18pp; Japanese.
 XX CC The present sequence represents a gene coding Chlamydia 16S ribosome RNA from Chlamydia psittaci. Also described in the present invention are: (1) a recombinant vector containing the above gene; and (2) a transformant transformed by the above recombinant vector. The nucleic acid, and primers which can hybridise to it, are used for the specific nucleic acid amplification detection of a Chlamydia genus microbe i.e. detection of PCR products.
 XX SQ Sequence 1548 BP; 415 A; 328 C; 451 G; 354 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 1548;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGGAGGATGACG 20
 DB 1178 GGAGGAAGGCGGAGGATGACG 1197

RESULT 14
 AAS11031
 ID AAS11031 standard; DNA; 1548 BP.
 XX AC AAS11031;
 XX DT 06-AUG-2003 (revised)
 XX DT 24-OCT-2001 (first entry)
 XX DE Chlamydia trachomatis 16S ribosomal RNA gene.
 XX KW Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human; food grain supplement; livestock; poultry; therapeutic; ds.
 XX OS Chlamydia trachomatis.
 XX PN WO200142457-A2.
 XX PD 14-JUN-2001.
 XX PF 29-NOV-2000; 2000WO-US042391.
 XX PR 29-NOV-1999; 99US-0168150P.
 XX PA (AVIB-) AVI BIOPHARMA INC.
 XX PI Iversen PL;
 XX DR WPI; 2001-457295/49.
 XX PT Antibacterial compound, useful for treating bacterial infections and as livestock and poultry food supplement, comprises antisense oligonucleotides complementary to bacterial 16S and 23S rRNA.
 XX PS Disclosure; Page; 62pp; English.
 XX CC AAS11021-AAS11034 represent the coding sequences of bacterial 16S ribosomal RNA (rRNA) genes. The sequences were used to design anti-

CC bacterial compounds comprising substantially uncharged antisense
CC oligomers containing 8-40 nucleotide subunits, including a targeting
CC nucleic acid sequence at least 10 nucleotides in length which is
CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The
CC antisense oligomers are used for treating a bacterial infection in a
CC human or a mammalian animal produced by *Escherichia coli*, *Salmonella*
CC typhimurium, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria*
CC gonorrhoea, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*
CC influenza, *Shigella dysenteriae*, *Staphylococcus aureus*, *Mycobacterium*
CC tuberculosis, *Streptococcus pneumoniae*, *Treponema pallidum* and *Chlamydia*
CC trachomatis. The antibacterial compound may be used as a food grain
CC supplement in livestock and poultry food composition. Note: The present
CC sequence is not shown in the specification but has been accessed from
CC GenBank using the appropriate accession number given in the
CC specification. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 1548 BP; 402 A; 327 C; 468 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGGAGGCGGAGGATGACG 20
Db 1179 GGAGGAGGCGGAGGATGACG 1198

RESULT 15

AAV66851
ID AAV66851 standard; DNA; 1549 BP.

AC AAV66851;

XX
DT 06-JAN-1999 (first entry)

XX
DE Chlamydia 16S ribosome RNA gene #7.

XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.

XX
OS Chlamydia trachomatis.

XX
PN JP10262679-A.

XX
PD 06-OCT-1998.

XX
PF 28-MAR-1997; 97JP-00078591.

XX
PR 28-MAR-1997; 97JP-00078591.

XX
PA (ATAT-) A & T KK.

XX
PA (TOKU) TOKUYAMA SODA KK.

XX
DR WPI; 1998-587294/50.

XX
FT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.

XX
PS Claim 1; Page 16-17; 18pp; Japanese.

XX
CC The present sequence represents a gene coding Chlamydia 16S ribosome RNA
CC from Chlamydia trachomatis. Also described in the present invention are:
CC (1) a recombinant vector containing the above gene; and (2) a
CC transformant transformed by the above recombinant vector. The nucleic
CC acid, and primers which can hybridise to it, are used for the specific
CC nucleic acid amplification detection of a Chlamydia genus microbe i.e.
CC detection of PCR products

XX
SQ Sequence 1549 BP; 402 A; 326 C; 470 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1549;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGGAGGCGGAGGATGACG 20
Db 1179 GGAGGAGGCGGAGGATGACG 1198
Search completed: August 4, 2004, 06:43:35
Job time : 166.337 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1393.25 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-1

Perfect score: 20

Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mas:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	20	100.0	122	9 AI903353	AI903353 RC-BT029-
c 2	20	100.0	133	10 BE084285	BE084285 PM3-BT065
c 3	20	100.0	168	14 CF199424	CF199424 EST1023 T
c 4	20	100.0	174	14 CD088408	CD088408 MCL-0050T

c	5	20	100.0	186	10	AW947763
	6	20	100.0	205	14	CD164995
	7	20	100.0	214	14	H74424
c	8	20	100.0	221	9	AT000468
	9	20	100.0	243	28	BH831104
	10	20	100.0	248	14	CF338988
	11	20	100.0	275	13	EX000722
c	12	20	100.0	297	12	EG874702
c	13	20	100.0	301	12	EG874706
c	14	20	100.0	312	9	AI903266
c	15	20	100.0	312	9	AI903386
c	16	20	100.0	312	9	AI903431
c	17	20	100.0	312	9	AI903433
	18	20	100.0	332	12	BI742715
	19	20	100.0	335	9	AI903432
c	20	20	100.0	335	10	BF810332
	21	20	100.0	338	9	AI903307
c	22	20	100.0	343	12	EG875496
c	23	20	100.0	350	10	BF810203
	24	20	100.0	366	12	EG987045
	25	20	100.0	368	9	AI903306
	26	20	100.0	373	12	EG988274
c	27	20	100.0	375	14	CD097562
	28	20	100.0	382	10	BF810198
c	29	20	100.0	382	14	CD164371
	30	20	100.0	391	10	BE427958
	31	20	100.0	394	28	BH819649
c	32	20	100.0	399	10	BF910944
c	33	20	100.0	407	13	BQ352721
c	34	20	100.0	409	10	AW804622
c	35	20	100.0	425	12	EG874668
	36	20	100.0	437	28	BH835798
	37	20	100.0	440	9	AU284247
	38	20	100.0	447	12	BM130023
	39	20	100.0	447	12	BM130070
c	40	20	100.0	454	14	CD091084
	41	20	100.0	464	14	CD032934
	42	20	100.0	465	12	EG357866
	43	20	100.0	470	12	BI744229
	44	20	100.0	473	28	BH831257
c	45	20	100.0	476	9	AU165135

ALIGNMENTS

RESULT 1
AI903353/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

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AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

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AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

AI903353 RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence. EST 30-MAR-2000

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-113_1.ht
m&t3=100199&t4=1)
Seq primer: puc 18 forward.

FEATURES
source
Location/Qualifiers
1..122
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT029"
/note="Organ: breast; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACAGGATTAGATACCC 20
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Db 100 GCAACACAGGATTAGATACCC 81

RESULT 2
BE084285
LOCUS
DEFINITION
PM3-BT0654-030300-002-d12 BT0654 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BE084285
VERSION
BE084285.1 GI:8474639
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 133)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F.F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=PM3-BT0654-030
300-002-d12&t3=2000-03-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 133.

FEATURES
source
Location/Qualifiers
1..133
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0654"
/note="Organ: breast; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 100.0%; Score 20; DB 10; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACAGGATTAGATACCC 20
|||||
Db 21 GCAACACAGGATTAGATACCC 40

RESULT 3
CF199424/c
LOCUS
DEFINITION
EST1023 Tamariix androssowii leaf Tamariix androssowii cDNA, mRNA sequence.
ACCESSION
CF199424
VERSION
CF199424.1 GI:33393797
KEYWORDS
EST.
SOURCE
Tamariix androssowii
ORGANISM
Tamariix androssowii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Tamaricaceae; Tamariix.
REFERENCE
1 (bases 1 to 168)
Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
EST acquired from cDNA library of Tamariix androssowii treated with NAHCO3
Unpublished (2003)
Contact: Yucheng Wang
Forestry Source and Environment College
Northeast Forestry University
Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
Tel: 086-451-2190607
Email: WANGYUCHENG1029@YAHOO.COM.CN.

FEATURES
source
Location/Qualifiers
1..168
/organism="Tamariix androssowii"
/mol_type="mRNA"
/db_xref="taxon:189785"
/tissue_type="leaf"
/clone_lib="Tamariix androssowii leaf"

ORIGIN
Query Match 100.0%; Score 20; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACAGGATTAGATACCC 20
|||||
Db 108 GCAACACAGGATTAGATACCC 89

RESULT 4
CD088408
LOCUS
DEFINITION
MCI-0050T-R112-C03-U.G MCI-0050 Schistosoma mansoni cDNA clone
MCI-0050T-R112-C03.G, mRNA sequence.
ACCESSION
CD088408

```

VERSION          CD088408.1  GI:34639304
KEYWORDS         EST.
SOURCE           Schistosoma mansoni
ORGANISM         Schistosoma mansoni

REFERENCE
AUTHORS          Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
                  Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
                  Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
                  Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
                  Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
                  Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
                  Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
                  Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
                  Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
TITLE            Transcriptome analysis of the acelomate human parasite Schistosoma
                  mansoni
JOURNAL          Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE          22879926
COMMENT          Contact: Dr. Sergio Verjovski-Almeida
                  Departamento de Bioquimica
                  Instituto de Quimica - Universidade de Sao Paulo
                  Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                  Brasil
                  Tel: +55-11-3091-2173
                  Fax: +55-11-3091-2186
                  Email: verjo@iq.usp.br
                  This sequence was derived from the FAPESP Schistosoma mansoni EST
                  Genome Project. All sequences in the project were assembled and
                  annotated. This entry and all the assembled sequences can be seen
                  in the following URL http://bioinfo.iq.usp.br/schisto/
                  Plate: MCL-0050T-R112 row: 3 column: C.
FEATURES         Location/Qualifiers
                  1..174
                    /organism="Schistosoma mansoni"
                    /mol_type="mRNA"
                    /db_xref="taxon:6183"
                    /clone="MCL-0050T-R112-C03.G"
                    /sex="mixed pool"
                    /dev_stage="cercaria"
                    /lab_host="Biomphalaria glabrata"
                    /clone_lib="MCL-0050"
                    /note="Vector: pGEM T-easy"
ORIGIN
Query Match      100.0%; Score 20; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
    |||||||
DB 74 GCAACACAGGATTAGATACCC 93

RESULT 5
AW947763/c
LOCUS            AW947763      186 bp      mRNA      linear      EST 31-MAY-2000
DEFINITION      RC0-MT0006-110300-021-d10 MT0006 Homo sapiens cDNA, mRNA sequence.
ACCESSION       AW947763
VERSION         AW947763.1  GI:8125537
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zagai, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Query Match      100.0%; Score 20; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
    |||||||
DB 74 GCAACACAGGATTAGATACCC 93

RESULT 6
CD164995
LOCUS            CD164995      205 bp      mRNA      linear      EST 14-SEP-2003
DEFINITION      MLI-0093T-D139-B11-U.G MLI-0093 Schistosoma mansoni cDNA clone
                  MLI-0093T-D139-B11-G, mRNA sequence.
ACCESSION       CD164995
VERSION         CD164995.1  GI:34701658
KEYWORDS        EST.
SOURCE          Schistosoma mansoni
ORGANISM        Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 205)
Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
JOURNAL          Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE          22879926
COMMENT          Contact: Dr. Sergio Verjovski-Almeida
                  Departamento de Bioquimica

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TITLE            Shotgun sequencing of the human transcriptome with ORF expressed
                  sequence tags
JOURNAL          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE          20202663
PUBMED          10737800
COMMENT          Contact: Simpson A.J.G.
                  Laboratory of Cancer Genetics
                  Ludwig Institute for Cancer Research
                  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                  Brazil
                  Tel: +55-11-2704922
                  Fax: +55-11-2707001
                  Email: asimpson@ludwig.org.br
                  This sequence was derived from the PAPESP/LICR Human Cancer Genome
                  Project. This entry can be seen in the following URL
                  (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RCO-MT0006-110
                  300-021-d10&t3=2000-03-11&t4=1)
                  Seq primer: puc 18 forward
                  High quality sequence start: 20
                  High quality sequence stop: 186.
FEATURES         Location/Qualifiers
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                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /dev_stage="Adult"
                    /clone_lib="MT0006"
                    /note="Organ: marrow; Vector: puc18; Site: 1: SmaI; Site 2:
                    SmaI; A mini-library was made by cloning products derived
                    from ORESTES PCR (U.S. Letters Patent application No.
                    196,716 - Ludwig Institute for Cancer Research) profiles
                    into the pUC 18 vector. Reverse transcription of tissue
                    mRNA and cDNA amplification were performed under low
                    stringency conditions."
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
    |||||||
DB 101 GCAACACAGGATTAGATACCC 82

RESULT 6
CD164995
LOCUS            CD164995      205 bp      mRNA      linear      EST 14-SEP-2003
DEFINITION      MLI-0093T-D139-B11-U.G MLI-0093 Schistosoma mansoni cDNA clone
                  MLI-0093T-D139-B11-G, mRNA sequence.
ACCESSION       CD164995
VERSION         CD164995.1  GI:34701658
KEYWORDS        EST.
SOURCE          Schistosoma mansoni
ORGANISM        Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 205)
Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,
Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
JOURNAL          Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE          22879926
COMMENT          Contact: Dr. Sergio Verjovski-Almeida
                  Departamento de Bioquimica

```

Instituto de Quimica - Universidade de Sao Paulo
 Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
 Brasil
 Tel: +55-11-3091-2173
 Fax: +55-11-3091-2186
 Email: verj@iq.usp.br

This sequence was derived from the PAPESP Schistosoma mansoni EST
 Genome Project. All sequences in the project were assembled and
 annotated. This entry and all the assembled sequences can be seen
 in the following URL <http://bioinfo.iq.usp.br/schisto/>
 Plate: ML1-0093T-D139 row: 11 column: B.

FEATURES

Location/Qualifiers
 1..205
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="ML1-0093T-D139-B11.G"
 /sex="mixed pool"
 /dev_stage="miracidium"
 /clone_lib="ML1-0093"
 /note="Vector: pGEM T-easy"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 205;
 Best Local Similarity 100.0%; Pred. No. 0.082;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACAGGATTAGATACCC 20

Db 57 GCAACAGGATTAGATACCC 76

RESULT 7

H74424 126 Standard Brassica napus cdNA clone R185F, mRNA sequence.
 DEFINITION 214 bp mRNA linear EST 31-OCT-1995
 H74424
 ACCESSION
 VERSION H74424.1 GI:1048331

KEYWORDS

SOURCE EST.

ORGANISM

Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 214)
 Park, Y.S., Kwak, J.M., Kwon, O.Y., Kim, Y.S., Lee, D.S., Cho, M.J.,
 Lee, H.H. and Nam, H.G.

Generation of expressed sequence tags of random root cDNA clones of
 Brassica napus by single-run partial sequencing

Plant Physiol. 103, 359-370 (1993)

94302145

MEDLINE

PUBMED

8029332

COMMENT

Contact: Nam, HG
 Plant Molecular Genetics Laboratory
 Pohang University of Science and Technology
 Dept. of Life Science, San31 Hyojadong, Pohang Kyungbuk 790-784,
 Korea

Tel: 825622792111

Fax: 825622792199

Email: nam@vision.postech.ac.kr

Seq primer: M13 forward.

FEATURES

Location/Qualifiers

1..214

/organism="Brassica napus"

/mol_type="mRNA"

/strain="L. cv Naeahan"

/db_xref="taxon:3708"

/clone="R185F"

/lab_host="E. coli DH5a"

/clone_lib="Standard"

/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; ESTs
 were generated from the root cDNA library of Brassica
 napus. The cDNA was synthesized from root poly(A) RNA

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 214;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACAGGATTAGATACCC 20

Db 124 GCAACAGGATTAGATACCC 143

RESULT 8

AT000468/c

LOCUS

DEFINITION

AT000468

CDNA clone DGT85, mRNA sequence.

ACCESSION

AT000468

VERSION

AT000468.1

GI:3414002

KEYWORDS

SOURCE EST.

ORGANISM

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 221)

Kwak, J.M., Kim, S.A., Hong, S.W. and Nam, H.G.

Evaluation of 515 expressed sequence tags obtained from guard cells

of Brassica campestris

Planta 202 (1), 9-17 (1997)

97320163

MEDLINE

PUBMED

9177047

COMMENT

Contact: Hong-Gil Nam

Department of Life Science, Plant Molecular Genetics Laboratory

Pohang University of Science and Technology

San 31 Hyojadong, Pohang Kyungbuk 790-784, Korea

Email: hgn@bric.postech.ac.kr

Submitted through BRIC(Biological Research Information Center) of

Korea URL: <http://bric.postech.ac.kr/>.

Location/Qualifiers

1..221

/organism="Brassica rapa subsp. pekinensis"

/mol_type="mRNA"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="DGT85"

/cell_type="guard cell protoplast"

/clone_lib="Brassica rapa guard cell"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 221;

Best Local Similarity 100.0%; Pred. No. 0.083;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACAGGATTAGATACCC 20

Db 119 GCAACAGGATTAGATACCC 100

RESULT 9

BH831104

LOCUS

DEFINITION

BH831104

CDNA clone DGT85, mRNA sequence.

ACCESSION

BH831104

VERSION

BH831104.1

GI:21028448

KEYWORDS

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

with Pharmacia's cDNA synthesis kit using oligo(dT) as a
 primer. The Eco RI/Not I adaptor was ligated to the
 dsDNA. The cDNA inserts were cloned into the pUC19
 vector digested with EcoRI."

BH831104 243 bp DNA linear GSS 20-MAY-2002
 BACPP32-L04.2 Pristionchus pacificus BAC ends Pristionchus
 pacificus genomic, genomic survey sequence.

BH831104.1 GI:21028448

KEYWORDS

SOURCE

ORGANISM

Pristionchus pacificus

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

```

REFERENCE
AUTHORS  Neodiplogasteridae; Pristionchus.
          1 (bases 1 to 243)
          Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar R.,
          Raddatz G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
          Jesse,T., Willare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE     A BAC-based genetic linkage map of the nematode Pristionchus
          pacificus
JOURNAL   Unpublished (2002)
COMMENT   Contact: Sommer RJ
          Evolutionary Biology
          Max-Planck-Institute for Developmental Biology
          Spemannstr. 37-39, Tuebingen D-72076, Germany
          Tel: 00497071601371
          Fax: 00497071601498
          Email: ralf.sommer@tuebingen.mpg.de
          Class: BAC ends.
FEATURES
source    Location/Qualifiers
          1..243
             /organism="Pristionchus pacificus"
             /mol_type="genomic DNA"
             /strain="var. California"
             /db_xref="taxon:54126"
             /clone_lib="Pristionchus pacificus BAC ends"
ORIGIN
Query Match      100.0%; Score 20; DB 28; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.084; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY  1 GCAACAGGATTAGATACCC 20
    |||||
Db  121 GCAACAGGATTAGATACCC 140

RESULT 10
CF338988      248 bp mRNA linear EST 18-AUG-2003
LOCUS         RCL1--03-G23.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION   Oryza sativa cDNA clone RCL1--03-G23, mRNA sequence.
ACCESSION    CF338988
VERSION      CF338988.1 GI:33826360
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL      Contact: Nahm B.H.
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source    Location/Qualifiers
          1..248
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="RCL1--03-G23"
             /tissue_type="callus"
             /dev_stage="proliferated callus on 2N6 media for 30 days"
             /lab_host="E.coli SOLR"
             /clone_lib="Regenerated callus lambda phage cDNA library
              (RCL1)"
             /notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
              XhoI; cDNA was inserted into lambda Uni-ZAP XR vector" at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"
ORIGIN
Query Match      100.0%; Score 20; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.084; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY  1 GCAACAGGATTAGATACCC 20
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Db  159 GCAACAGGATTAGATACCC 178

RESULT 11
BX000722      275 bp mRNA linear EST 03-DEC-2002
LOCUS         BX000722 Pinus pinaster xylem Pinus pinaster cDNA clone PPEM56,
DEFINITION   mRNA sequence.
ACCESSION    BX000722
VERSION      BX000722.1 GI:26020290
KEYWORDS     EST.
SOURCE       Pinus pinaster
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE    Le Provost,G., Raiwa,J., Pot,D., Brach,J. and Plomion,P.
              Seasonal variation in transcript accumulation in wood forming
              tissue of maritime pine (Pinus pinaster Ait.) with emphasis on a
              cell wall Glycine Rich Protein
              Unpublished (2002)
JOURNAL      Contact: Frigerio JM
COMMENT      Genetique et Amelioration 69
              INRA
              route d'Arcachon 33612 Cestas CEDEX France
              Email: Frigerio@piereton.inra.fr.
FEATURES
source    Location/Qualifiers
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             /organism="Pinus pinaster"
             /mol_type="mRNA"
             /db_xref="taxon:71647"
             /clone="PPEM56"
             /tissue_type="xylem"
             /clone_lib="Pinus pinaster xylem"
             /notes="Compression wood was induced in four 14-year old
              maritime pine clones by artificial bending. Control clone
              (no bending) were sampled for xylem associated with early
              (August) of the growing seasons. Differentiating xylem
              corresponding to Early wood, late wood, compression wood
              and opposite wood were used for mRNA fingerprinting using
              the cDNA-AFLPP assay."
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"
ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 275;
Best Local Similarity 100.0%; Pred. No. 0.085; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY  1 GCAACAGGATTAGATACCC 20
    |||||
Db  99 GCAACAGGATTAGATACCC 118

RESULT 12
BG874702/c     297 bp mRNA linear EST 30-MAY-2001
LOCUS         CM0-BN0075-220200-237-h05 EN0075 Homo sapiens cDNA, mRNA sequence.
DEFINITION   BG874702
ACCESSION    BG874702
VERSION      BG874702.1 GI:14251633
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Ngai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

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Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM0-BN0075-220>)

200-237-h05&t3=2000-02-22&t4=1

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 297.

FEATURES

source

1..297

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BN0075"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 297;

Best Local Similarity 100.0%; Pred. No. 0.086;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACACAGGATTAGATACCC 20

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Db 198 GCACACAGGATTAGATACCC 179

RESULT 13

BG874706/c

LOCUS

DEFINITION CM3-BN0075-240200-101-h05 BN0075 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG874706

VERSION BG874706.1 GI:14251637

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 301)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Ngai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

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Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-BN0075-240>)

200-101-h05&t3=2000-02-24&t4=1

Seq primer: puc 18 forward

High quality sequence start: 19

High quality sequence stop: 301.

FEATURES

source

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/db_xref="taxon:9606"

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/clone_lib="BN0075"

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Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 301;

Best Local Similarity 100.0%; Pred. No. 0.086;

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Db 202 GCACACAGGATTAGATACCC 183

RESULT 14

AI903266/c

LOCUS

DEFINITION RC-BT029-070199-018 BT029 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI903266

VERSION AI903266.1 GI:6493653

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 312)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Ngai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

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20202663

10737800

COMMENT

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Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-018.html
 &t3=070199&t4=1)
 Seq primer: puc 18 forward.

FEATURES

Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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/note="Organ: Breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 312;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
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 Db 100 GCAACACAGGATTAGATACCC 81

RESULT 15

AI903386/c 312 bp mRNA linear EST 30-MAR-2000
 LOCUS RC-BT029-110199-165 BT029 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AI903386
 VERSION AI903386.1 GI:6493773

KEYWORDS

EST.

SOURCE

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 312)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT029-165.html
 &t3=110199&t4=1)

Seq primer: puc 18 forward.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /sex="female"
 /dev_stage="Adult"
 /clone_lib="BT029"

/note="Organ: Breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 312;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
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 Db 100 GCAACACAGGATTAGATACCC 81

Search completed: August 4, 2004, 09:20:47
 Job time : 1397.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:32:11 ; Search time 1825.78 Seconds
(without alignments)
385.436 Million cell updates/sec

Title: US-09-940-860-1

Perfect score: 20

Sequence: 1 gcaacagattagataccc 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 37577330 seqs, 17593059518 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	25	54	US-10-715-220-1
5	20	100.0	30	39	US-09-940-860-6
6	20	100.0	47	6	US-08-246-935-2
7	20	100.0	50	49	US-10-343-313-76
8	20	100.0	50	49	US-10-343-313-77
9	20	100.0	50	49	US-10-343-313-79
10	20	100.0	50	49	US-10-343-313-80
11	20	100.0	50	49	US-10-343-313-81
12	20	100.0	50	49	US-10-343-313-82
13	20	100.0	50	49	US-10-343-313-83
14	20	100.0	50	49	US-10-343-313-84
15	20	100.0	50	49	US-10-343-313-85
16	20	100.0	50	49	US-10-343-313-87
17	20	100.0	50	49	US-10-343-313-88
18	20	100.0	50	49	US-10-343-313-89
19	20	100.0	50	49	US-10-343-313-90
20	20	100.0	50	49	US-10-343-313-91
21	20	100.0	50	49	US-10-343-313-98
22	20	100.0	50	49	US-10-343-313-99
23	20	100.0	50	49	US-10-343-313-102
24	20	100.0	50	49	US-10-343-313-104
25	20	100.0	50	49	US-10-343-313-105
26	20	100.0	105	51	US-10-415-182A-337
27	20	100.0	237	11	US-08-731-034-686
28	20	100.0	237	56	US-60-004-674-686
29	20	100.0	248	11	US-08-731-034-37
30	20	100.0	248	56	US-60-004-674-37
31	20	100.0	279	51	US-10-417-884-3170
32	20	100.0	279	51	US-10-417-884-3171
33	20	100.0	293	51	US-10-410-040A-19
34	20	100.0	294	51	US-10-410-040A-15
35	20	100.0	294	51	US-10-410-040A-16
36	20	100.0	294	51	US-10-410-040A-17
37	20	100.0	294	51	US-10-410-040A-18
38	20	100.0	294	51	US-10-410-040A-20
39	20	100.0	294	51	US-10-410-040A-21
40	20	100.0	294	51	US-10-410-040A-23
41	20	100.0	306	13	US-09-107-433-2236
42	20	100.0	306	53	US-10-617-320-2236
43	20	100.0	352	58	US-60-029-960-1510
44	20	100.0	375	27	US-09-652-913-6226
45	20	100.0	413	20	US-09-465-877-1662

ALIGNMENTS

RESULT 1

US-09-940-860-1

Sequence 1, Application US/09940860

GENERAL INFORMATION:

APPLICANT: Rothman, Richard

APPLICANT: Majumdar, Maulik

TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

FILE REFERENCE: 01107.00185

CURRENT APPLICATION NUMBER: US/09/940,860

CURRENT FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/229,376

PRIOR FILING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

US-09-940-860-1

Query Match

Best Local Similarity

Matches

20

Conservative

0

Mismatches

0

Indels

0

Gaps

0

QY

1

GCAACACAGGATTAGATACCC

20

DB

1

GCAACACAGGATTAGATACCC

20

RESULT 2

US-09-283-655-1

Sequence 1, Application US/09283655

GENERAL INFORMATION:

APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS

FILE REFERENCE: IMSCI.009A

CURRENT APPLICATION NUMBER: US/09/283,655

CURRENT FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide primer

US-09-283-655-1

Query Match

Best Local Similarity

Matches

20

Conservative

0

Mismatches

0

Indels

0

Gaps

0

QY

1

GCAACACAGGATTAGATACCC

20

DB

5

GCAACACAGGATTAGATACCC

24

RESULT 3

US-09-620-375-1

Sequence 1, Application US/09620375

GENERAL INFORMATION:

APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS

FILE REFERENCE: IMSCI.009A

CURRENT APPLICATION NUMBER: US/09/620,375

CURRENT FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: 09/283,655

PRIOR FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide primer

US-09-620-375-1

Query Match

Best Local Similarity

Matches

20

Conservative

0

Mismatches

0

Indels

0

Gaps

0

QY

1

GCAACACAGGATTAGATACCC

20

DB

5

GCAACACAGGATTAGATACCC

24

RESULT 4

US-09-620-375-1

Sequence 1, Application US/09620375

GENERAL INFORMATION:

APPLICANT: Vojdani, A.

TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS

FILE REFERENCE: IMSCI.009A

CURRENT APPLICATION NUMBER: US/09/620,375

CURRENT FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: 09/283,655

PRIOR FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide primer

US-09-620-375-1

Query Match

Best Local Similarity

Matches

20

Conservative

0

Mismatches

0

Indels

0

Gaps

0

QY

1

GCAACACAGGATTAGATACCC

20

DB

5

GCAACACAGGATTAGATACCC

24

```

US-10-715-220-1
; Sequence 1, Application US/10715220
; GENERAL INFORMATION:
; APPLICANT: Vojdani, A.
; TITLE OF INVENTION: DETECTION OF MYOPLASMA IN PATIENTS WITH
; FILE OF INVENTION: CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
; FILE REFERENCE: IMSCI.009A
; CURRENT APPLICATION NUMBER: US/10/715,220
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/283,655
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1:
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-715-220-1

Query Match      100.0%; Score 20; DB 54; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
Db 5 GCAACACAGGATTAGATACCC 24

RESULT 5
US-09-940-860-6
; Sequence 6, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6:
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-6

Query Match      100.0%; Score 20; DB 39; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
Db 2 GCAACACAGGATTAGATACCC 21

RESULT 6
US-08-246-935-2/c
; Sequence 2, Application US/08246935
; GENERAL INFORMATION:
; APPLICANT: Weisburg, William G.
; APPLICANT: Lane, David J.
; TITLE OF INVENTION: A METHOD FOR DETECTING AND IDENTIFYING
; FILE OF INVENTION: PATHOGENIC ORGANISMS USING TARGET SEQUENCES AS DETECTORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

```

```

; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/246,935
; APPLICATION NUMBER: US/08/246,935
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/707,646
; FILING DATE: 30-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: GTR90-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)861-6240
; TELEFAX: (617)861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA probe
; FEATURE:
; NAME/KEY: GTS OLIGO NUMBER 1739
US-08-246-935-2

Query Match      100.0%; Score 20; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
Db 33 GCAACACAGGATTAGATACCC 14

RESULT 7
US-10-343-319-76
; Sequence 76, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76:
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76

Query Match      100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
|
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 8

US-10-343-319-77
; Sequence 77, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Treponema denticola
US-10-343-319-77

Query Match 100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
|
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 9

US-10-343-319-79
; Sequence 79, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Leptothrix mobilis
US-10-343-319-79

Query Match 100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
|
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 10

US-10-343-319-80
; Sequence 80, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Thiomicrospira denitrificans
US-10-343-319-80

Query Match 100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
|
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 11

US-10-343-319-81
; Sequence 81, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-319-81

Query Match 100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
|
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 12

US-10-343-319-82
; Sequence 82, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.

```
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Actinobacillus actinomycetemcomitans
US-10-343-319-82
```

```
Query Match          100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
```

```
QY 1 GCAACAGGATTAGATACCC 20
Db 16 GCAACAGGATTAGATACCC 35
|||||
```

RESULT 13

```
US-10-343-319-83
; Sequence 83, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-343-319-83
```

```
Query Match          100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
```

```
QY 1 GCAACAGGATTAGATACCC 20
Db 16 GCAACAGGATTAGATACCC 35
|||||
```

RESULT 14

```
US-10-343-319-84
; Sequence 84, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
```

```
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-343-319-84
```

```
Query Match          100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
```

```
QY 1 GCAACAGGATTAGATACCC 20
Db 16 GCAACAGGATTAGATACCC 35
|||||
```

RESULT 15

```
US-10-343-319-85
; Sequence 85, Application US/10343319
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Salmonella typhi
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and
; OTHER INFORMATION: Rhodospirillum rubrum.
US-10-343-319-85
```

```
Query Match          100.0%; Score 20; DB 49; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCAACAGGATTAGATACCC 20
Db 16 GCAACAGGATTAGATACCC 35
|||||
```

```
Search completed: August 4, 2004, 11:29:48
Job time : 1826.78 secs
```

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1393.25 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggaggaagcgaggatgacg 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_esttc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	90.0	304	9 AV295422	AV295422 RH1Z2.23
2	18	90.0	410	12 BG102240	BG102240 RH1Z2.23
3	18	90.0	508	12 BG380134	BG380134 UI-R-GS0-
4	18	90.0	530	29 CG093861	CG093861 PUF3X26TB

c	5	18	90.0	567	29	CG093863
c	6	18	90.0	573	14	CA199884
c	7	18	90.0	617	14	CA236557
c	8	18	90.0	784	29	CG657309
c	9	18	90.0	784	29	CG734728
c	10	18	90.0	826	10	BE743778
c	11	18	90.0	867	29	CG458612
c	12	18	90.0	890	28	BZ803618
c	13	18	90.0	951	29	CG038934
c	14	18	90.0	972	29	CG038933
c	15	18	90.0	992	28	BZ803611
c	16	18	90.0	1013	28	BZ806256
c	17	17	85.0	242	9	AV319131
c	18	17	85.0	245	14	CF771463
c	19	17	85.0	255	9	AV324545
c	20	17	85.0	259	14	CA484206
c	21	17	85.0	261	14	CA486269
c	22	17	85.0	268	9	AI438796
c	23	17	85.0	273	14	CF760514
c	24	17	85.0	294	10	BB021190
c	25	17	85.0	303	10	AW202526
c	26	17	85.0	314	14	CD226821
c	27	17	85.0	317	9	AW066567
c	28	17	85.0	318	28	BH627207
c	29	17	85.0	322	10	BB040793
c	30	17	85.0	330	14	CA485170
c	31	17	85.0	332	28	BH229295
c	32	17	85.0	337	10	BB131766
c	33	17	85.0	338	10	BB161598
c	34	17	85.0	339	14	CF758969
c	35	17	85.0	339	14	CF758236
c	36	17	85.0	358	13	BQ282009
c	37	17	85.0	360	14	CB603914
c	38	17	85.0	361	14	CD670294
c	39	17	85.0	374	10	BF457064
c	40	17	85.0	389	14	CF487372
c	41	17	85.0	406	10	AW286184
c	42	17	85.0	409	12	BM266611
c	43	17	85.0	424	9	AI593552
c	44	17	85.0	426	9	AI941805
c	45	17	85.0	427	10	BF723566

ALIGNMENTS

RESULT 1
AV295422

LOCUS
DEFINITION

AV295422 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730434H04 3', similar to S68987 set=Set beta isoform
{alternatively spliced}, mRNA sequence.

ACCESSION
AV295422

VERSION
AV295422.1 GI:6327439

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 304)

Authors
Konno,H., Azawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,

Fukuda,S., Fukunishi,Y., Harai,A., Hayatsu,N., Hirozane,T., Hori,F.,

Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,

Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,

Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,

Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,

Suzuki,H., Suzuki,H., Takahashi,F., Tatenno,M., Tomiwa,N.,

Tsunoda,Y., Watanabe,S., Yamamura,T., Yasunishi,A.,

Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al. 1999)

Unpublished (1999)

CONTACT: Yoshihide Hayashizaki

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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES source
1. 304
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="573043H04"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 8 days embryo"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATTCGAGTTAATTAATCCCTCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAATTAATCCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN
Query Match 90.0%; Score 18; DB 9; Length 304;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGGAGGCGGAGGATCA 18
Db 94 GGAGGAGGCGGAGGATCA 111
RESULT 2
BG102240/c
LOCUS
DEFINITION RH122_23_H01.b1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
sequence.
ACCESSION BG102240
VERSION BG102240.1 GI:12617185
KEYWORDS EST.
SOURCE Sorghum propinquum
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 410)
Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.
An EST database from Sorghum: Sorghum propinquum rhizomes Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 377
POLYA=No.
FEATURES Location/Qualifiers
1. 410
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RH122)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector Lambda Zap II. Clones to be sequenced were prepared by mass excision."

ORIGIN
Query Match 90.0%; Score 18; DB 12; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAGGAGGCGGAGGATCA 18
Db 251 GGAGGAGGCGGAGGATCA 234
RESULT 3
BG380134/c
LOCUS
DEFINITION UI-R-CS0-btp-d-11-0-UI-s1 UI-R-CS0 Rattus norvegicus cDNA clone
UI-R-CS0-btp-d-11-0-UI 3', mRNA sequence.
ACCESSION BG380134
VERSION BG380134.1 GI:13304606
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road 4156 MEERF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: benton-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive

elements were found in this cDNA sequence: 1-23,
 >AT_rich#Low complexity
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES

source
 1. .508
 /location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CS0-btp-d-11-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CS0"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CS0
 library is a normalized library constructed from the
 following rat heart tissues: embryonic day 17, embryonic
 day 19, embryonic day 21, adult day 1, adult day 12, adult
 day 75, adult day 200. For a detailed description of the
 library from which this clone was derived, please visit
 our web site at ratest.eng.uiowa.edu. The subtraction has
 been previously described in (Bonaldo, Lennon and Soares,
 Genome Research 6:791-806, 1996)
 TAG TISSUE=rat heart pool
 TAG LIB=UI-R-CS0
 TAG_SEQ=ATAAGATAAC"

ORIGIN

Query Match 90.0%; Score 18; DB 12; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAGGAAGGCGAGGATGAC 19
 |||||
 Db 349 GAGGAAGGCGAGGATGAC 332

RESULT 4

CG093861
 LOCUS PUF5X26TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
 DEFINITION genomic survey sequence.
 ACCESSION CG093861
 VERSION CG093861.1 GI:33976155
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 530)

REFERENCE
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J., and
 Bennetzen,J.

TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Other_GSSs: PUF5X26TD
 Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES

source
 1. .530
 /location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBTa0725F04"

/clone_lib="ZM_0.6_1.0_KB"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN

Query Match 90.0%; Score 18; DB 29; Length 530;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGGAAGCGGAGGATGA 18
 |||||
 Db 117 GGAGGAAGCGGAGGATGA 134

RESULT 5

CG093863/c
 LOCUS PUF5X26TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
 DEFINITION genomic survey sequence.

ACCESSION CG093863
 VERSION CG093863.1 GI:33976157
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 567)

REFERENCE
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J., and
 Bennetzen,J.

TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Other_GSSs: PUF5X26TB
 Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.

FEATURES

source
 1. .567
 /location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
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 /clone_lib="ZM_0.6_1.0_KB"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN

Query Match 90.0%; Score 18; DB 29; Length 567;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAGGAAGCGGAGGATGA 18
 |||||
 Db 415 GGAGGAAGCGGAGGATGA 398

RESULT 6

CA199884/c
 LOCUS SCLFL1013D09.g FL1 Saccharum officinarum cDNA clone SCLFL1013D09
 DEFINITION 5', mRNA sequence.

ACCESSION CA199884
 VERSION CA199884.1 GI:35232591
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE

1 (bases 1 to 573)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCSEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P

AUTHORS

Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089

TITLE

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br

JOURNAL

Plate: 013 row: D column: 09

COMMENT

Seq primer: T7 Promoter Primer.

FEATURES

source

1..573
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSBLFL1013D09"
/lab_host="DH10B"
/clone_lib="FL1"

/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Inflorescence at beginning of development (1cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucust.lad.ic.unicamp.br/public"

ORIGIN

Query Match 90.0%; Score 18; DB 14; Length 573;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 GAGGAGCGGAGGATGAC 19

|||||

Db 419 GAGGAGCGGAGGATGAC 402

RESULT 7

CA236557/c

LOCUS

DEFINITION CA236557 617 bp mRNA linear EST 25-SEP-2003
cDNA clone SCSBFL5014E09.9 Saccharum officinarum FL5 Saccharum officinarum

ACCESSION

CA236557

VERSION

CA236557.1 GI:35306233

KEYWORDS

EST.

SOURCE

Saccharum officinarum

ORGANISM

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 617)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCSEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..617

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCSBLFL5014E09"

/lab_host="DH10B"

/clone_lib="Saccharum officinarum FL5"

/note="Organ: Developed inflorescence (20cm-long) without rachis; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Developed inflorescence (20cm-long) without rachis]. cDNA was

prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were

fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were

directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at

http://sucust.lad.ic.unicamp.br/public"

ORIGIN

Query Match 90.0%; Score 18; DB 14; Length 617;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGAGGAGCGGAGGATGAC 18

|||||

Db 255 GGAGGAGCGGAGGATGAC 238

RESULT 8

CC657309/c

LOCUS

DEFINITION CC657309 784 bp DNA linear GSS 19-JUN-2003
CGJAO16TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0295D07,
genomic survey sequence.

ACCESSION

CC657309

VERSION

CC657309.1 GI:32060634

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 784)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: 1P

Class: sheared ends.

Location/Qualifiers

1..784

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBMA0295D07"

/clone_lib="ZM_0.7_1.5_KB"

/note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

ORIGIN

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Query Match      90.0%; Score 18; DB 29; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGGAGGATGA 18
    |||||
Db 484 GGAGGAAGCGGAGGATGA 467

RESULT 9
CG734728/c
LOCUS      784 bp      DNA      linear      GSS 22-OCT-2003
DEFINITION ZMMBBb0290C20.f ZMMBBb Zea mays subsp. mays genomic clone
ACCESSION  ZMMBBb0290C20 5', genomic survey sequence.
VERSION
KEYWORDS
SOURCE
ORGANISM    Zea mays subsp. mays (maize)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
            and Wing, R.
            Sequencing of the maize genome
            Unpublished (2003)
            Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0290 row: C column: 20
Seq primer: T7
Class: BAC ends.
            Location/Qualifiers
            1..784
            /organism="Zea mays subsp. mays"
            /mol_type="genomic DNA"
            /cultivar="B73"
            /sub_species="mays"
            /db_xref="taxon:4578"
            /clone="ZMMBBb0290C20"
            /lab_host="DH10B"
            /note="Vector: pBelcBAC11; Site 1: HindIII; Site 2:
            HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match      90.0%; Score 18; DB 29; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGGAGGATGA 18
    |||||
Db 478 GGAGGAAGCGGAGGATGA 461

RESULT 10
BE743778
LOCUS      826 bp      mRNA      linear      EST 15-SEP-2000
DEFINITION 601577866F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926924 5',
            mRNA sequence.
ACCESSION  BE743778
VERSION
KEYWORDS
            EST.

```

```

SOURCE
ORGANISM    Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: DCTD/BTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LCM755 row: k column: 21
            High quality sequence stop: 771.
            Location/Qualifiers
            1..826
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3926924"
            /tissue_type="adenocarcinoma cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_9"
            /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match      90.0%; Score 18; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAAGCGGAGGATGAC 19
    |||||
Db 598 GAGGAAGCGGAGGATGAC 615

RESULT 11
CG458612
LOCUS      867 bp      DNA      linear      GSS 17-SEP-2003
DEFINITION FUIKZ64TD ZM_0.6_1.0 KB Zea mays genomic clone ZMMBtra0607K08,
            genomic survey sequence.
ACCESSION  CG458612
VERSION
KEYWORDS
SOURCE
ORGANISM    Zea mays
            Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 867)
            Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Reanick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
            Bennetzen, J.
            Maize Genomics Consortium
            Unpublished (2003)
            Other GSSs: FUIKZ64TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TP

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  ACCESSION
    BZ803618
  VERSION
    BZ803618.1 GI:29012224
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  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 890)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUFDX67TB
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TP
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  VERSION
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    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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  1 (bases 1 to 972)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUFBL28TD
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TP
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  SOURCE
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    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
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  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUFBL28TD
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
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  VERSION
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    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 951)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUFBL28TB
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
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    CG038933.1 GI:33911089
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    Zea mays
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    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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  1 (bases 1 to 972)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
  Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other GSSs: PUFBL28TD
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
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DB 830 GGAGGAAGCGGAGGATGA 847

RESULT 15

BZ803611
LOCUS PUFDX677B ZM 0.6_1.0_KB Zea mays genomic clone ZMBTa297K14,
DEFINITION 992 bp DNA linear GSS 17-MAR-2003
genomic survey sequence.

ACCESSION BZ803611
VERSION BZ803611.1 GI:29012211
KEYWORDS GSS.

SOURCE

Zea mays
Zea mays
Zukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 992)

REFERENCE

AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.

TITLE

Maize Genomics Consortium
Unpublished (2003)

JOURNAL

COMMENT Other GSSs: PUFDX67TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 199.036 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-1

Perfect score: 20

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	20	100.0	279	7	US-10-417-884A-3170		Sequence 3170, Ap
C 2	20	100.0	279	7	US-10-417-884A-3171		Sequence 3171, Ap
C 3	20	100.0	442	7	US-10-793-479-14013		Sequence 14013, A
C 4	20	100.0	600	8	US-10-148-328B-74		Sequence 74, Appl
C 5	20	100.0	601	8	US-10-148-328B-75		Sequence 75, Appl
C 6	20	100.0	755	1	PCT-IL04-000351-5		Sequence 5, Appl
C 7	20	100.0	895	8	US-10-486-307-5		Sequence 5, Appl
C 8	20	100.0	1113	8	US-10-148-328B-70		Sequence 70, Appl
C 9	20	100.0	1197	8	US-10-148-328B-100		Sequence 100, Appl
C 10	20	100.0	1210	8	US-10-148-328B-81		Sequence 81, Appl
C 11	20	100.0	1223	8	US-10-148-328B-66		Sequence 66, Appl
C 12	20	100.0	1225	8	US-10-148-328B-71		Sequence 71, Appl
C 13	20	100.0	1233	8	US-10-148-328B-58		Sequence 98, Appl
C 14	20	100.0	1236	8	US-10-148-328B-76		Sequence 76, Appl
C 15	20	100.0	1237	8	US-10-148-328B-67		Sequence 67, Appl
C 16	20	100.0	1250	8	US-10-148-328B-92		Sequence 92, Appl
C 17	20	100.0	1250	8	US-10-148-328B-104		Sequence 104, Appl
C 18	20	100.0	1269	8	US-10-148-328B-60		Sequence 60, Appl
C 19	20	100.0	1276	8	US-10-148-328B-95		Sequence 95, Appl
C 20	20	100.0	1281	8	US-10-148-328B-106		Sequence 106, Appl
C 21	20	100.0	1288	8	US-10-148-328B-64		Sequence 64, Appl
C 22	20	100.0	1288	8	US-10-148-328B-73		Sequence 73, Appl
C 23	20	100.0	1292	8	US-10-148-328B-84		Sequence 84, Appl
C 24	20	100.0	1296	8	US-10-148-328B-91		Sequence 91, Appl

ORGANISM: Enterococcus faecium
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SEQUENCE DESCRIPTION: SEQ ID NO: 3170:
US-10-417-884A-3170

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Qy 1 GCAAACAGGATTAGATACCC 20
Db 134 GCAAACAGGATTAGATACCC 115

RESULT 2
US-10-417-884A-3171/c
Sequence 3171, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A. Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER: READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3171:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...279
SEQUENCE DESCRIPTION: SEQ ID NO: 3171:
US-10-417-884A-3171

Query Match 100.0%; Score 20; DB 7; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
Db 134 GCAAACAGGATTAGATACCC 115

RESULT 3
US-10-793-479-14013
Sequence 14013, Application US/10793479
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/10/793,479
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US/09/513,999
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14013
LENGTH: 442
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 363
OTHER INFORMATION: s=g or c
US-10-793-479-14013

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
Db 288 GCAAACAGGATTAGATACCC 307

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US-10-148-328B-74
Sequence 74, Application US/10148328B
GENERAL INFORMATION:
APPLICANT: JEANNIN, PASCALE
APPLICANT: FERNODET, JEAN-LUC
APPLICANT: GUERINEAU, MICHEL
APPLICANT: SIMONET, PASCAL
TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
TITLE OF INVENTION: OF NOVEL COMPOUNDS
FILE REFERENCE: 03806.0547-00000
CURRENT APPLICATION NUMBER: US/10/148,328B
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: FR9915032
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/FR00/03311
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/209,800
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 74
LENGTH: 600
TYPE: DNA
ORGANISM: Unknown organism
FEATURE:
OTHER INFORMATION: Origin of the sequence: soil organism
FEATURE:
NAME/KEY: modified_base
LOCATION: (494)

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; OTHER INFORMATION: variable nucleotide
US-10-148-328B-74

Query Match      100.0%; Score 20; DB 8; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 265 GCAACACAGGATTAGATACCC 284

RESULT 5
US-10-148-328B-75
; Sequence 75, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 75
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-75

Query Match      100.0%; Score 20; DB 8; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 265 GCAACACAGGATTAGATACCC 284

RESULT 6
PCT-IL04-00351-5/c
; Sequence 5, Application PC/TIL0400351
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Eugene
; APPLICANT: Ron, Elcira Z.
; APPLICANT: Koren, Orry
; TITLE OF INVENTION: BIOREMEDIATION OF PETROLEUM POLLUTION USING WATER-INSOLUBLE URIC
; FILE REFERENCE: 27821
; CURRENT APPLICATION NUMBER: PCT/IL04/00351
; CURRENT FILING DATE: 2004-04-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Acinetobacter sp. strain OK1
PCT-IL04-00351-5

Query Match      100.0%; Score 20; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 0.019;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 696 GCAACACAGGATTAGATACCC 677

RESULT 7
US-10-486-307-5/c
; Sequence 5, Application US/10486307
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours, Inc.
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: CLI789 PCT
; CURRENT APPLICATION NUMBER: US/10/486,307
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Brachyomonas sp. CHX
US-10-486-307-5

Query Match      100.0%; Score 20; DB 8; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
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Db 664 GCAACACAGGATTAGATACCC 645

RESULT 8
US-10-148-328B-70
; Sequence 70, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 70
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-70

Query Match      100.0%; Score 20; DB 8; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
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Db 574 GCAACACAGGATTAGATACCC 593
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RESULT 9
US-10-148-328B-100
; Sequence 100, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 100
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-100

Query Match      100.0%; Score 20; DB 8; Length 1197;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAACAGGATTAGATACCC 20
Db      642 GCAAACAGGATTAGATACCC 661

RESULT 10
US-10-148-328B-81
; Sequence 81, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 81
; LENGTH: 1210
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-81

Query Match      100.0%; Score 20; DB 8; Length 1210;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-10-148-328B-66
; Sequence 66, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-66

Query Match      100.0%; Score 20; DB 8; Length 1223;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAACAGGATTAGATACCC 20
Db      638 GCAAACAGGATTAGATACCC 657

RESULT 12
US-10-148-328B-71
; Sequence 71, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 71
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-71

Query Match      100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  GCAAACAGGATTAGATACCC 20
Db      616 GCAAACAGGATTAGATACCC 635

RESULT 11
US-10-148-328B-66
; Sequence 66, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-66

Query Match      100.0%; Score 20; DB 8; Length 1223;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAACAGGATTAGATACCC 20
Db      638 GCAAACAGGATTAGATACCC 657

RESULT 12
US-10-148-328B-71
; Sequence 71, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 71
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-71

Query Match      100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-148-328B-71
Query Match      100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
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Db 641 GCAACACAGGATTAGATACCC 660

RESULT 13
US-10-148-328B-98
; Sequence 98, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
; NAME/KEY: modified_base
; LOCATION: (435)
; OTHER INFORMATION: variable nucleotide
US-10-148-328B-98

Query Match      100.0%; Score 20; DB 8; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 644 GCAACACAGGATTAGATACCC 663

RESULT 14
US-10-148-328B-76
; Sequence 76, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
; NAME/KEY: modified_base
; LOCATION: (435)
; OTHER INFORMATION: variable nucleotide
US-10-148-328B-76

Query Match      100.0%; Score 20; DB 8; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 648 GCAACACAGGATTAGATACCC 667

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; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 76
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-76

Query Match      100.0%; Score 20; DB 8; Length 1236;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 653 GCAACACAGGATTAGATACCC 672

RESULT 15
US-10-148-328B-67
; Sequence 67, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-67

Query Match      100.0%; Score 20; DB 8; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
   |||||
Db 648 GCAACACAGGATTAGATACCC 667

Search completed: August 4, 2004, 11:43:43
Job time : 200.036 secs
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 199.036 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggaggagcgagatgacg 20

Scoring table: OLIGO_NUC

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Searched: 4754066 seqs, 1232178907 residues

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Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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9: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	18	90.0	2551	US-10-425-115-29000	Sequence 29000, A
C 3	17	85.0	700	US-10-425-115-109468	Sequence 109468, A
C 4	17	85.0	1073	US-10-473-974-43	Sequence 43, Appl
C 5	17	85.0	1847	US-10-767-701-14989	Sequence 14989, A
C 6	17	85.0	2097	US-10-425-115-151508	Sequence 151508, A
C 7	16	80.0	352	US-10-425-115-130914	Sequence 130914, A
C 8	16	80.0	407	US-10-767-701-22770	Sequence 22770, A
C 9	16	80.0	510	US-10-767-701-28210	Sequence 28210, A
C 10	16	80.0	551	US-10-425-115-38956	Sequence 38956, A
C 11	16	80.0	677	US-10-425-115-122047	Sequence 122047, A
C 12	16	80.0	788	US-10-425-115-126075	Sequence 126075, A
C 13	16	80.0	1601	US-10-425-115-158496	Sequence 158496, A
C 14	16	80.0	5536	US-10-221-714B-297	Sequence 297, Appl
C 15	15	75.0	144	US-10-674-124A-38	Sequence 38, Appl
C 16	15	75.0	201	US-60-582-609-23584	Sequence 23584, A
C 17	15	75.0	201	US-60-582-609-35417	Sequence 35417, A
C 18	15	75.0	285	US-10-767-701-30539	Sequence 30539, A
C 19	15	75.0	290	US-10-430-201-4831	Sequence 4831, Appl
C 20	15	75.0	290	US-10-430-201-4832	Sequence 4832, Appl
C 21	15	75.0	383	US-10-425-115-169825	Sequence 169825, A
C 22	15	75.0	390	US-10-779-543-13155	Sequence 13155, A
C 23	15	75.0	400	US-10-779-543-12976	Sequence 12976, A
C 24	15	75.0	412	US-10-425-115-48631	Sequence 48631, A

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C 25 15 75.0 441 6 US-10-425-115-70573 Sequence 70573, A
C 26 15 75.0 454 7 US-10-767-701-22517 Sequence 22517, A
C 27 15 75.0 547 5 US-09-397-206A-4333 Sequence 4333, Appl
C 28 15 75.0 554 6 US-10-425-115-125836 Sequence 125836, A
C 29 15 75.0 561 6 US-10-425-115-160109 Sequence 160109, A
C 30 15 75.0 697 6 US-10-425-115-98986 Sequence 98986, A
C 31 15 75.0 781 6 US-10-425-115-136893 Sequence 136893, A
C 32 15 75.0 788 7 US-10-363-345A-26387 Sequence 26387, A
C 33 15 75.0 788 7 US-10-363-345A-26388 Sequence 26388, A
C 34 15 75.0 824 6 US-10-425-115-121769 Sequence 121769, A
C 35 15 75.0 889 7 US-10-620-246-5 Sequence 5, Appli
C 36 15 75.0 907 6 US-10-425-115-4377 Sequence 4377, Appl
C 37 15 75.0 916 7 US-10-363-345A-21759 Sequence 21759, A
C 38 15 75.0 916 7 US-10-363-345A-21760 Sequence 21760, A
C 39 15 75.0 927 7 US-10-363-345A-40085 Sequence 40085, A
C 40 15 75.0 927 7 US-10-363-345A-40086 Sequence 40086, A
C 41 15 75.0 976 6 US-10-425-115-103979 Sequence 103979, A
C 42 15 75.0 1123 6 US-10-425-115-153306 Sequence 153306, A
C 43 15 75.0 1175 7 US-10-767-701-13151 Sequence 13151, A
C 44 15 75.0 1303 6 US-10-425-115-99222 Sequence 99222, A
C 45 15 75.0 1316 7 US-10-767-701-13537 Sequence 13537, A

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ALIGNMENTS

RESULT 1

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US-10-425-115-28998/c
; Sequence 28998, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 28998
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(850)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126457C.1
US-10-425-115-28998

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Query Match 90.0%; Score 18; DB 6; Length 850;
Best Local Similarity 100.0%; Pred.No. 0.71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGGAGCGGAGGATGA 18
    |||||
DB 617 GGAGGAGCGGAGGATGA 600

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RESULT 2

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US-10-425-115-29000
; Sequence 29000, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 29000
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126459C.1
US-10-425-115-29000

Query Match      90.0%; Score 18; DB 6; Length 2551;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGAGGCGGAGGATGA 18
Db      1853 GGAGGAGGCGGAGGATGA 1870

RESULT 3
US-10-425-115-109468/c
; Sequence 109468, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 109468
; LENGTH: 700
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_31330C.1
US-10-425-115-109468

Query Match      85.0%; Score 17; DB 6; Length 700;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GAGGAGGCGGAGGATGA 18
Db      188 GAGGAGGCGGAGGATGA 172

RESULT 4
US-10-473-974-43
; Sequence 43, Application US/10473974
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAWADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/10/473,974
; CURRENT FILING DATE: 2003-10-03
; PRIOR FILING DATE: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 43
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-473-974-43

Query Match      85.0%; Score 17; DB 7; Length 1073;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGAGGCGGAGGATG 17
Db      1005 GGAGGAGGCGGAGGATG 1021

RESULT 5
US-10-767-701-14989
; Sequence 14989, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14989
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS9317_1
US-10-767-701-14989

Query Match      85.0%; Score 17; DB 7; Length 1847;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GAGGAAGCGGAGGATGA 18
Db      1631 GAGGAAGCGGAGGATGA 1647

RESULT 6
US-10-425-115-151508
; Sequence 151508, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 151508
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(2097)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_69698C.1
US-10-425-115-151508

Query Match      85.0%; Score 17; DB 6; Length 2097;
Best Local Similarity 100.0%; Pred. No. 2.6;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGAAGCGGAGGATCA 18
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Db 1592 GAGGAAGCGGAGGATCA 1608

RESULT 7
US-10-425-115-130914
; Sequence 130914, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 130914
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_50875C.1
US-10-425-115-130914

Query Match 80.0%; Score 16; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GAAGCGGAGGATGAGC 20
    |||||
Db 251 GAAGCGGAGGATGAGC 266

RESULT 8
US-10-767-701-22770/c
; Sequence 22770, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 22770
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14513702
US-10-767-701-22770

Query Match 80.0%; Score 16; DB 7; Length 407;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGAAGCGGAGGATG 17
    |||||
Db 167 GAGGAAGCGGAGGATG 152

RESULT 9
US-10-767-701-28210
; Sequence 28210, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28210
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7535963
US-10-767-701-28210

Query Match 80.0%; Score 16; DB 7; Length 510;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGAAGCGGAGGAT 16
    |||||
Db 466 GGAGGAAGCGGAGGAT 481

RESULT 10
US-10-425-115-38956
; Sequence 38956, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 38956
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(551)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135529C.1
US-10-425-115-38956

Query Match 80.0%; Score 16; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGAAGCGGAGGAT 16
    |||||
Db 390 GGAGGAAGCGGAGGAT 405

RESULT 11
US-10-425-115-122047/c
; Sequence 122047, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 122047
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_42791C.1
US-10-425-115-122047

Query Match 80.0%; Score 16; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAGGCGGAGGATG 17
|||||
DB 415 GAGGAGGCGGAGGATG 400

RESULT 12

US-10-425-115-126075/c
; Sequence 126075, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 126075
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_4644C.1
US-10-425-115-126075

Query Match 80.0%; Score 16; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAAGGCGAGGATGACG 20
|||||
DB 254 GAAGGCGAGGATGACG 239

RESULT 13

US-10-425-115-158496/c
; Sequence 158496, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 158496
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76128C.1
US-10-425-115-158496

Query Match 80.0%; Score 16; DB 6; Length 1601;
Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGAGGCGGAGGATG 17
|||||
DB 350 GAGGAGGCGGAGGATG 335

RESULT 14

US-10-221-714B-297
; Sequence 297, Application US/10221714B
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 297
; LENGTH: 5536
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-221-714B-297

Query Match 80.0%; Score 16; DB 6; Length 5536;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGGCGGAGGAT 16
|||||
DB 1968 GGAGGAGGCGGAGGAT 1983

RESULT 15

US-10-674-124A-38/c
; Sequence 38, Application US/10674124A
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JF00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 38
; LENGTH: 144

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DIS07_10007639
; FEATURE:
; OTHER INFORMATION: Located on chromosome 1
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 5692908
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 188636
US-10-674-124A-38

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Query Match      75.0%; Score 15; DB 7; Length 144;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGAGGAAGCGGAGGA 15
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Db      28 GGAGGAAGCGGAGGA 14

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Job time : 200.036 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 180.964 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-1

Perfect score: 20

Sequence: 1 gcaaacaggattagatacc 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	11	US-09-940-860-1
2	20	100.0	25	17	US-10-715-220-1
3	20	100.0	30	11	US-09-940-860-6
4	20	100.0	50	12	US-10-343-319-76
5	20	100.0	50	12	US-10-343-319-77
6	20	100.0	50	12	US-10-343-319-79
7	20	100.0	50	12	US-10-343-319-80
8	20	100.0	50	12	US-10-343-319-81
9	20	100.0	50	12	US-10-343-319-82
10	20	100.0	50	12	US-10-343-319-83
11	20	100.0	50	12	US-10-343-319-84
12	20	100.0	50	12	US-10-343-319-85
13	20	100.0	50	12	US-10-343-319-87
14	20	100.0	50	12	US-10-343-319-88

15	20	100.0	50	12	US-10-343-319-89	Sequence 89, Appl
16	20	100.0	50	12	US-10-343-319-90	Sequence 90, Appl
17	20	100.0	50	12	US-10-343-319-91	Sequence 91, Appl
18	20	100.0	50	12	US-10-343-319-98	Sequence 98, Appl
19	20	100.0	50	12	US-10-343-319-99	Sequence 99, Appl
20	20	100.0	50	12	US-10-343-319-102	Sequence 102, Appl
21	20	100.0	50	12	US-10-343-319-104	Sequence 104, Appl
22	20	100.0	50	12	US-10-343-319-105	Sequence 105, Appl
23	20	100.0	293	17	US-10-410-040A-19	Sequence 19, Appl
24	20	100.0	294	17	US-10-410-040A-15	Sequence 15, Appl
25	20	100.0	294	17	US-10-410-040A-16	Sequence 16, Appl
26	20	100.0	294	17	US-10-410-040A-17	Sequence 17, Appl
27	20	100.0	294	17	US-10-410-040A-18	Sequence 18, Appl
28	20	100.0	294	17	US-10-410-040A-20	Sequence 20, Appl
29	20	100.0	294	17	US-10-410-040A-21	Sequence 21, Appl
30	20	100.0	294	17	US-10-410-040A-23	Sequence 23, Appl
31	20	100.0	549	10	US-09-991-936-1717	Sequence 1717, Ap
32	20	100.0	571	9	US-09-879-536-755	Sequence 755, App
33	20	100.0	624	9	US-09-879-536-728	Sequence 728, App
34	20	100.0	665	9	US-09-879-536-476	Sequence 476, App
35	20	100.0	672	9	US-09-879-536-450	Sequence 450, App
36	20	100.0	856	15	US-10-213-878-5	Sequence 5, Appli
37	20	100.0	856	15	US-10-214-059-5	Sequence 5, Appli
38	20	100.0	895	15	US-10-230-026-5	Sequence 5, Appli
39	20	100.0	1009	9	US-09-900-876-1	Sequence 1, Appli
40	20	100.0	1070	9	US-09-737-297-2	Sequence 2, Appli
41	20	100.0	1140	9	US-09-737-297-5	Sequence 5, Appli
42	20	100.0	1208	9	US-09-894-467-1	Sequence 1, Appli
43	20	100.0	1320	15	US-10-168-337A-7	Sequence 7, Appli
44	20	100.0	1322	15	US-10-168-337A-5	Sequence 5, Appli
45	20	100.0	1335	15	US-10-029-397A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-940-860-1
; Sequence 1, Application US/09940860
; Publication No. US2004000555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-1

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAAACAGGATTAGATACCC 20
|||||
Db 1 GCAAAACAGGATTAGATACCC 20

RESULT 2
US-10-715-220-1
; Sequence 1, Application US/10715220
; Publication No. US20040077015A1
; GENERAL INFORMATION:

APPLICANT: Voidani, A.
TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
FILE REFERENCE: INSCI.009A
CURRENT FILING DATE: 2003-11-17
PRIOR FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US/09/283,655
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-715-220-1
Query Match 100.0%; Score 20; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAAACAGGATTAGATACCC 20
DB 5 GCAAAACAGGATTAGATACCC 24
RESULT 3
US-09-940-860-6
Sequence 6, Application US/09940860
Publication No. US2004000555A1
GENERAL INFORMATION:
APPLICANT: Rothman, Richard
APPLICANT: Majumdar, Maulik
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
FILE REFERENCE: 01107.00185
CURRENT APPLICATION NUMBER: US/09/940,860
CURRENT FILING DATE: 2001-08-29
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 60/229,376
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic amplification primer
US-09-940-860-6
Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAAACAGGATTAGATACCC 20
DB 2 GCAAAACAGGATTAGATACCC 21
RESULT 4
US-10-343-319-76
Sequence 76, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933

PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: AU PQ09090/2000
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 76
LENGTH: 50
TYPE: DNA
ORGANISM: Campylobacter jejuni
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76
Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAAACAGGATTAGATACCC 20
DB 16 GCAAAACAGGATTAGATACCC 35
RESULT 5
US-10-343-319-77
Sequence 77, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: AU PQ09090/2000
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 50
TYPE: DNA
ORGANISM: Treponema denticola
FEATURE:
OTHER INFORMATION:
US-10-343-319-77
Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAAAACAGGATTAGATACCC 20
DB 16 GCAAAACAGGATTAGATACCC 35
RESULT 6
US-10-343-319-79
Sequence 79, Application US/10343319
Publication No. US20040072242A1
GENERAL INFORMATION:
APPLICANT: Hunter, Neil
APPLICANT: Jacques, Nicholas A.
APPLICANT: Martin, Fjelda E.
APPLICANT: Nardkani, Mangala A.
TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
FILE REFERENCE: DAVI139.002APC
CURRENT APPLICATION NUMBER: US/10/343,319
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/AU01/00933
PRIOR FILING DATE: 2001-07-27

```
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Leptothrix mobilis
US-10-343-319-79

Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACAGGATTAGATACCC 20
Db 16 GCAAAACAGGATTAGATACCC 35

RESULT 7
US-10-343-319-80
; Sequence 80, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Thiomicrospira denitrificans
US-10-343-319-80

Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACAGGATTAGATACCC 20
Db 16 GCAAAACAGGATTAGATACCC 35

RESULT 8
US-10-343-319-81
; Sequence 81, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
```

```
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-319-81

Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACAGGATTAGATACCC 20
Db 16 GCAAAACAGGATTAGATACCC 35

RESULT 9
US-10-343-319-82
; Sequence 82, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Actinobacillus actinomycetemcomitans
US-10-343-319-82

Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAAACAGGATTAGATACCC 20
Db 16 GCAAAACAGGATTAGATACCC 35

RESULT 10
US-10-343-319-83
; Sequence 83, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-343-319-83
```

```
Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20: Conservative 0; Mismatches 0 Indels
```

Qy 1 GCAACAGGATTAGATACCC 20
|||
Db 16 GCAACAGGATTAGATACCC 35

```

RESULT 11
US-10-343-319-84
; Sequence 84, Application US10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjeida E.
; APPLICANT: Nardkani, Margala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-343-319-84

```

```
Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
```

Qy 1 GCAAACAGGATTAGATACCC 20
Dp 16 GCAAACAGGATTAGATACCC 35

```

RESULT 12
US-10-343-319-85
; Sequence 85, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Salmonella typhi
; FEATURE:
; NAME/KEY: misc:feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and
; OTHER INFORMATION: Rhodospirillum rubrum.
US-10-343-319-85

```

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels

Qy 1 GCAAACAGGATTAGATACCC 20
|||
Db 16 GCAAACAGGATTAGATACCC 35

```

RESULT 13
US-10-343-319-87
; Sequence 87, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjeida E. A.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ09090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Legionella pneumophila
US-10-343-319-87

```

```
Query Match      100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels
```

Qy 1 GCAAACAGGATTAGATACCC 20
|||
Db 16 GCAAACAGGATTAGATACCC 35

```

RESULT 14
US-10-343-319-88
; Sequence 88, Application US/10343319
; Publication No. US2004007242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda B.
; APPLICANT: Nardkani, Margala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Caulobacter vibrioides
US-10-343-319-88

```

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels

QY 1 GCAACAGGATTAGATACCC 20

Db 16 GCAACACAGGATTAGATACCC 35

```

RESULT 15
US-10-343-319-89
; Sequence 89, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAV1139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Nitrobacter winogradskyi
US-10-343-319-89

```

Query Match 100.0%; Score 20; DB 12; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
 Db 16 GCAACACAGGATTAGATACCC 35

Search completed: August 4, 2004, 11:56:21
 Job time : 180.964 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 180.964 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggaggaggcggaggatgacg 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	11	US-09-940-860-2
2	20	100.0	30	11	US-09-940-860-7
3	20	100.0	1548	9	US-09-726-774-11
4	20	100.0	1548	17	US-10-719-633-11
5	20	100.0	1550	11	US-09-940-860-5
6	20	100.0	1230025	16	US-10-289-762-1
7	18	90.0	2123	13	US-10-425-114-4575
8	18	90.0	2738	17	US-10-437-963-25445
9	17	85.0	1143	17	US-10-437-963-4673
10	17	85.0	1305	13	US-10-425-114-32946
11	17	85.0	2124	13	US-10-425-114-32781
12	17	85.0	2145	16	US-10-369-493-35514
13	16	80.0	338	13	US-10-425-114-25403
14	16	80.0	1251	13	US-10-282-122A-17957

c 15	16	80.0	1543	13	US-10-425-114-15476
c 16	16	80.0	1554	13	US-10-425-114-3338
c 17	16	80.0	1594	13	US-10-425-114-15935
c 18	16	80.0	3962	17	US-10-437-963-72402
c 19	16	80.0	5536	13	US-10-221-714A-297
c 20	15	80.0	5536	13	US-10-311-455-1805
c 21	15	75.0	168	17	US-10-437-963-26084
c 22	15	75.0	178	9	US-09-923-876-5759
c 23	15	75.0	178	11	US-09-923-876-5759
c 24	15	75.0	236	12	US-09-922-293-666
c 25	15	75.0	254	12	US-09-922-293-989
c 26	15	75.0	266	12	US-09-922-293-504
c 27	15	75.0	274	12	US-09-922-293-509
c 28	15	75.0	281	9	US-09-922-293-873
c 29	15	75.0	281	12	US-09-922-293-506
c 30	15	75.0	293	12	US-09-922-293-508
c 31	15	75.0	294	9	US-09-924-093B-5844
c 32	15	75.0	313	17	US-10-437-963-67279
c 33	15	75.0	318	17	US-10-437-963-68928
c 34	15	75.0	320	12	US-09-922-293-503
c 35	15	75.0	357	9	US-09-770-791-589
c 36	15	75.0	405	9	US-09-867-701-4895
c 37	15	75.0	421	10	US-09-814-353-14381
c 38	15	75.0	455	10	US-09-814-353-1641
c 39	15	75.0	455	10	US-09-814-353-7997
c 40	15	75.0	499	13	US-10-342-887-2152
c 41	15	75.0	499	13	US-10-172-118-2152
c 42	15	75.0	525	9	US-09-938-842A-2377
c 43	15	75.0	525	11	US-09-938-842A-2377
c 44	15	75.0	543	17	US-10-437-963-4676
c 45	15	75.0	585	13	US-10-027-632-236613

ALIGNMENTS

RESULT 1

US-09-940-860-2

; Sequence 2, Application US/09940860

; Publication No. US2004000555A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, Richard

; APPLICANT: Majumdar, Maulik

; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA

; FILE REFERENCE: 01107.00185

; CURRENT APPLICATION NUMBER: US/09/940.860

; CURRENT FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/229,376

; PRIOR FILING DATE: 2000-08-31

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic amplification primer

US-09-940-860-2

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGGCGGAGGATGACG 20
|||||

Db 1 GGAGGAGGCGGAGGATGACG 20
|||||

RESULT 2

US-09-940-860-7

; Sequence 7, Application US/09940860

; Publication No. US2004000555A1

; GENERAL INFORMATION:

```
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-7
```

```
Query Match      100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGAGGAAGCGGAGGATGACG 20
          |||||
Db       3 GGAGGAAGCGGAGGATGACG 22
```

RESULT 3

```
US-09-726-774-11
; Sequence 11, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-726-774-11
```

```
Query Match      100.0%; Score 20; DB 9; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGAGGAAGCGGAGGATGACG 20
          |||||
Db       1179 GGAGGAAGCGGAGGATGACG 1198
```

RESULT 4

```
US-10-719-633-11
; Sequence 11, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-10-719-633-11
```

```
Query Match      100.0%; Score 20; DB 17; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGAGGAAGCGGAGGATGACG 20
          |||||
Db       1179 GGAGGAAGCGGAGGATGACG 1198
```

RESULT 5

```
US-09-940-860-5
; Sequence 5, Application US/09940860
; Publication No. US2004000555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-940-860-5
```

```
Query Match      100.0%; Score 20; DB 11; Length 1550;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGAGGAAGCGGAGGATGACG 20
          |||||
Db       1179 GGAGGAAGCGGAGGATGACG 1198
```

RESULT 6

```
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(15000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15001)-(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
```

```
QY      1 GGAGGAAGCGGAGGATGACG 20
          |||||
Db       1179 GGAGGAAGCGGAGGATGACG 1198
```



```
FEATURE:
NAME/KEY: misc feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
```

Query Match 100.0%; Score 20; DB 16; Length 1230025;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAGGAAGCGGAGGATGACG 20
      |||||
Db 1011866 GGAGGAAGCGGAGGATGACG 1011885
```

```
RESULT 7
US-10-425-114-4575/c
; Sequence 4575, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114-4575
```

Query Match 90.0%; Score 18; DB 13; Length 2123;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAGGAAGCGGAGGATGCA 18
      |||||
+Db 305 GGAGGAAGCGGAGGATGCA 288
```

```
RESULT 8
US-10-437-963-25445/c
; Sequence 25445, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 25445
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445
```

Query Match 90.0%; Score 18; DB 17; Length 2738;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAGGAAGCGGAGGATCA 18
      |||||
Db 614 GGAGGAAGCGGAGGATCA 597
```

```
RESULT 9
US-10-437-963-4673
; Sequence 4673, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4673
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11535C.1
US-10-437-963-4673
```

Query Match 85.0%; Score 17; DB 17; Length 1143;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAGGAAGCGGAGGATG 17
      |||||
Db 816 GGAGGAAGCGGAGGATG 832
```

RESULT 10

US-10-425-114-32946
; Sequence 32946, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32946
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017043F07_FLI
US-10-425-114-32946

Query Match 85.0%; Score 17; DB 13; Length 1305;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAAGCGGAGGATGA 18
|||||
DB 1122 GAGGAAGCGGAGGATGA 1138

RESULT 11

US-10-425-114-32781/c
; Sequence 32781, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32781
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017021D09_FLI
US-10-425-114-32781

Query Match 85.0%; Score 17; DB 13; Length 2124;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAAGCGGAGGATGA 18
|||||
DB 190 GAGGAAGCGGAGGATGA 174

RESULT 12

US-10-369-493-35514/c
; Sequence 35514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35514
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35514

Query Match 85.0%; Score 17; DB 16; Length 2145;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAAGCGGAGGATGA 18
|||||
DB 900 GAGGAAGCGGAGGATGA 884

RESULT 13

US-10-425-114-25403
; Sequence 25403, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25403
; LENGTH: 338
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3898-009-B5_FLI
US-10-425-114-25403

Query Match 80.0%; Score 16; DB 13; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAAGCGGAGGATGACG 20
|||||
DB 237 GAAGCGGAGGATGACG 252

RESULT 14

US-10-282-122A-17957
; Sequence 17957, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17957
LENGTH: 1251
TYPE: DNA
ORGANISM: *Corynebacterium diptheriae*
US-10-282-122A-17957

Query Match 80.0%; Score 16; DB 13; Length 1251;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGAAGCGGAGGATG 17
|||||
DB 403 GAGGAAGCGGAGGATG 418

RESULT 15
US-10-425-114-15476/c
Sequence 15476, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15476
LENGTH: 1543
TYPE: DNA
ORGANISM: *Zea mays*
FEATURE:
OTHER INFORMATION: Clone ID: LIB3060-007-A11_FLI
US-10-425-114-15476

Query Match 80.0%; Score 16; DB 13; Length 1543;

Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GAGGAAGCGGAGGATG 17
|||||
DB 330 GAGGAAGCGGAGGATG 315
Search completed: August 4, 2004, 11:56:24
Job time : 183.964 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:32:11 ; Search time 1825.78 Seconds
(without alignments)
385.436 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggagggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 50.0

Searched: 37577330 seqs, 17593059518 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:*
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- 14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:*
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- 17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:*
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- 19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:*
- 20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:*
- 21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:*
- 22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:*
- 23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:*
- 24: /cgn2_6/ptodata/2/pna/US095D COMB.seq:*
- 25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:*
- 26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:*
- 27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:*
- 28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:*
- 29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:*
- 30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:*
- 31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:*
- 32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:*
- 33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:*
- 34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:*
- 35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:*
- 36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:*
- 37: /cgn2_6/ptodata/2/pna/US099A COMB.seq:*
- 38: /cgn2_6/ptodata/2/pna/US099B COMB.seq:*
- 39: /cgn2_6/ptodata/2/pna/US099C COMB.seq:*
- 40: /cgn2_6/ptodata/2/pna/US099D COMB.seq:*
- 41: /cgn2_6/ptodata/2/pna/US099E COMB.seq:*
- 42: /cgn2_6/ptodata/2/pna/US099F COMB.seq:*
- 43: /cgn2_6/ptodata/2/pna/US100A COMB.seq:*

- 44: /cgn2_6/ptodata/2/pna/US100B COMB.seq:*
- 45: /cgn2_6/ptodata/2/pna/US101A COMB.seq:*
- 46: /cgn2_6/ptodata/2/pna/US101B COMB.seq:*
- 47: /cgn2_6/ptodata/2/pna/US102A COMB.seq:*
- 48: /cgn2_6/ptodata/2/pna/US102B COMB.seq:*
- 49: /cgn2_6/ptodata/2/pna/US103A COMB.seq:*
- 50: /cgn2_6/ptodata/2/pna/US103B COMB.seq:*
- 51: /cgn2_6/ptodata/2/pna/US104A COMB.seq:*
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- 68: /cgn2_6/ptodata/2/pna/US6012 COMB.seq:*
- 69: /cgn2_6/ptodata/2/pna/US6013 COMB.seq:*
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- 71: /cgn2_6/ptodata/2/pna/US6015 COMB.seq:*
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- 75: /cgn2_6/ptodata/2/pna/US6019 COMB.seq:*
- 76: /cgn2_6/ptodata/2/pna/US6020 COMB.seq:*
- 77: /cgn2_6/ptodata/2/pna/US6021 COMB.seq:*
- 78: /cgn2_6/ptodata/2/pna/US6022 COMB.seq:*
- 79: /cgn2_6/ptodata/2/pna/US6023A COMB.seq:*
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- 90: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:*
- 91: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:*
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- 93: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:*
- 94: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:*
- 95: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:*
- 96: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:*
- 97: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:*
- 98: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:*
- 99: /cgn2_6/ptodata/2/pna/US6042 COMB.seq:*
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- 101: /cgn2_6/ptodata/2/pna/US6044 COMB.seq:*
- 102: /cgn2_6/ptodata/2/pna/US6045 COMB.seq:*
- 103: /cgn2_6/ptodata/2/pna/US6046 COMB.seq:*
- 104: /cgn2_6/ptodata/2/pna/US6047 COMB.seq:*
- 105: /cgn2_6/ptodata/2/pna/US6048 COMB.seq:*
- 106: /cgn2_6/ptodata/2/pna/US6049 COMB.seq:*
- 107: /cgn2_6/ptodata/2/pna/US6050 COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	39	US-09-940-860-2
2	20	100.0	30	39	Sequence 2, Appli
3	20	100.0	1548	54	US-09-940-860-7
4	20	100.0	1550	39	Sequence 11, Appli
5	20	100.0	1038608	16	US-09-201-228A-1
6	20	100.0	1230025	48	US-10-283-782-1
7	20	100.0	1230230	20	US-09-438-185-1
8	20	100.0	1230230	20	US-09-438-185A-1
9	18	90.0	2123	47	US-10-219-999-18302
10	18	90.0	2123	51	US-10-425-114-4575
11	18	90.0	2123	51	US-10-425-114A-4575
12	18	90.0	2738	51	US-10-437-963-25445
13	18	90.0	13218	30	US-09-702-134-21825
14	18	90.0	13218	33	US-09-815-264-71774
15	18	90.0	13263	26	US-09-620-392-33867
16	17	85.0	231	16	US-09-236-218A-1587
17	17	85.0	231	40	US-09-955-568-1587
18	17	85.0	245	17	US-09-293-979A-2609
19	17	85.0	245	42	US-09-982-402-2609
20	17	85.0	245	64	US-60-085-146-2509
21	17	85.0	309	17	US-09-280-918A-596
22	17	85.0	309	63	US-60-079-469-696
23	17	85.0	313	35	US-09-873-402A-12532
24	17	85.0	313	76	US-60-209-830-12489
25	17	85.0	404	76	US-60-207-458-29567
26	17	85.0	410	76	US-60-207-458-3288
27	17	85.0	415	34	US-09-849-528A-17839
28	17	85.0	415	76	US-60-202-214-17594
29	17	85.0	430	76	US-60-207-458-48639
30	17	85.0	434	34	US-09-849-528A-29197
31	17	85.0	434	76	US-60-202-214-28952
32	17	85.0	440	34	US-09-849-528A-27635
33	17	85.0	440	76	US-60-202-214-27390
34	17	85.0	443	35	US-09-865-438A-49839
35	17	85.0	443	76	US-60-207-458-94095
36	17	85.0	448	19	US-09-394-745-50382
37	17	85.0	448	24	US-09-565-306-75437
38	17	85.0	458	27	US-09-654-617-272567
39	17	85.0	458	29	US-09-684-016-272567
40	17	85.0	475	27	US-09-654-617-454236
41	17	85.0	475	29	US-09-684-016-454236
42	17	85.0	502	25	US-09-617-682A-3766
43	17	85.0	548	35	US-09-865-419A-32915
44	17	85.0	548	35	US-09-865-419A-44146
45	17	85.0	548	76	US-60-208-063-15974

ALIGNMENTS

```

RESULT 1
US-09-940-860-2
; OTHER INFORMATION: synthetic amplification primer
; Sequence 2, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majumdar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-2
Query Match 100.0%; Score 20; DB 39; Length 20;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGCGGAGGATGACG 20
      |||||
Db 1 GGAGGAGCGGAGGATGACG 20
      |||||

RESULT 2
US-09-940-860-7
; Sequence 7, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majumdar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-7
Query Match 100.0%; Score 20; DB 39; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGCGGAGGATGACG 20
      |||||
Db 3 GGAGGAGCGGAGGATGACG 22
      |||||

RESULT 3
US-10-719-633-11
; Sequence 11, Application US/10719633
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-10-719-633-11
Query Match 100.0%; Score 20; DB 54; Length 1548;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGCGGAGGATGACG 20
      |||||
Db 1179 GGAGGAGCGGAGGATGACG 1198
      |||||

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RESULT 4

US-09-940-860-5
; Sequence 5, Application US/09940860
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 0107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Chlamydia trichomatis
US-09-940-860-5

Query Match 100.0%; Score 20; DB 39; Length 1550;
Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 1 GGAGGAAGCGGAGGATGACG 20
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Db 1179 GGAGGAAGCGGAGGATGACG 1198

RESULT 5

US-09-201-228A-1/c
; Sequence 1, Application US/09201228A
; GENERAL INFORMATION:
; APPLICANT: Griffais, Remy
; APPLICANT: Hoiseth, Susan K.
; APPLICANT: Zagursky, Robert John
; APPLICANT: Metcalf, Benjamin J.
; APPLICANT: Peek, Joel A.
; APPLICANT: Sankaran, Barunathi
; APPLICANT: Fletcher, Leah Diane
; TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
; TITLE OF INVENTION: AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
; TITLE OF INVENTION: PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
; FILE REFERENCE: 9710-0004-999
; CURRENT APPLICATION NUMBER: US/09/201,228A
; CURRENT FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/107,077
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: FR 97-16034
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: FR 97-15041
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 5981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1038608
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1038608)
; OTHER INFORMATION: n = A,T,C or G
US-09-201-228A-1

Query Match 100.0%; Score 20; DB 16; Length 1038608;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 1 GGAGGAAGCGGAGGATGACG 20
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Db 635877 GGAGGAAGCGGAGGATGACG 635858

RESULT 6

US-10-289-762-1
; Sequence 1, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(15000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15001)...(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30001)...(45000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45001)...(60000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60001)...(75000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (75001)...(90000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (90001)...(105000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (105001)...(120000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (120001)...(135000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (135001)...(150000)
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; NAME/KEY: misc feature
; LOCATION: (150001)...(165000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (165001)...(180000)
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; NAME/KEY: misc feature
; LOCATION: (180001)...(195000)
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (195001)...(210000)

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; LOCATION: (405001)..(420000)
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; NAME/KEY: misc feature
; LOCATION: (420001)..(435000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n=a or c or g or t

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; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
; LOCATION: (495001)..(510000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (510001)..(525000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (525001)..(540000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
; LOCATION: (540001)..(555000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (555001)..(570000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
; LOCATION: (585001)..(600000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (600001)..(615000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (615001)..(630000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
; LOCATION: (630001)..(645000)
; OTHER INFORMATION: n=a or c or g or t
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; NAME/KEY: misc feature
; LOCATION: (645001)..(660000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (660001)..(675000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (675001)..(690000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc feature

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Query Match 100.0%; Score 20; DB 48; Length 1230025;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGAGGATGACG 20
 |||||
 Db 1011866 GGAGGAAGCGAGGATGACG 1011885

RESULT 7
 US-09-438-185-1
 ; Sequence 1, Application US/09438185
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephens, Richard

```
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185
; CURRENT FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1230230
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1

Query Match          100.0%; Score 20; DB 20; Length 1230230;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGCAGGATGACG 20
DB 1001741 GGAGGAAGCGCAGGATGACG 1001760

RESULT 8
US-09-438-185A-1
; Sequence 1, Application US/09438185A
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1230230
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1

Query Match          100.0%; Score 20; DB 20; Length 1230230;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGCAGGATGACG 20
DB 1001741 GGAGGAAGCGCAGGATGACG 1001760

RESULT 9
US-10-219-999-18302/c
; Sequence 18302, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-10/52726/C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; CURRENT APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 18302
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (161)..(1768)
; OTHER INFORMATION:
US-10-219-999-18302

Query Match          90.0%; Score 18; DB 47; Length 2123;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGCAGGATGA 18
DB 305 GGAGGAAGCGCAGGATGA 288

RESULT 10
US-10-425-114-4575/c
; Sequence 4575, Application US/10425114
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21/53313/B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114-4575

Query Match          90.0%; Score 18; DB 51; Length 2123;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGCGCAGGATGA 18
DB 305 GGAGGAAGCGCAGGATGA 288

RESULT 11
US-10-425-114A-4575/c
; Sequence 4575, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-10/52726/C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; CURRENT APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 18302
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (161)..(1768)
; OTHER INFORMATION:
US-10-219-999-18302
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; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114A-4575

Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGAGGATGA 18
Db 305 GGAGGAAGGCGAGGATGA 288

RESULT 12
US-10-437-963-25445/c
; Sequence 25445, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yibua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 25445
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445

Query Match
Best Local Similarity 90.0%; Score 18; DB 51; Length 2738;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGAGGATGA 18
Db 614 GGAGGAAGGCGAGGATGA 597

RESULT 13
US-09-702-134-21825/c
; Sequence 21825, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 21825
; LENGTH: 13218
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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-21825

Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGAGGATGA 18
Db 103 GGAGGAAGGCGAGGATGA 86

RESULT 14
US-09-815-264-71774/c
; Sequence 71774, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 71774
; LENGTH: 13218
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-09-815-264-71774

Query Match
Best Local Similarity 90.0%; Score 18; DB 33; Length 13218;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAAGGCGAGGATGA 18
Db 103 GGAGGAAGGCGAGGATGA 86

RESULT 15
US-09-620-392-33867/c
; Sequence 33867, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 33867
; LENGTH: 13263
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-09-620-392-33867

Query Match
Best Local Similarity 90.0%; Score 18; DB 26; Length 13263;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGAGGAAGGCGAGGATGA 18
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Db 103 GGAGGAAGGCGAGGATGA 86

Search completed: August 4, 2004, 11:29:54
Job time : 1831.78 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 963.229 Seconds
(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-3

Perfect score: 22

Sequence: 1 acaagcccgagagatttca 22

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
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- 6: gb.pat.*
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- 8: gb.pl.*
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- 10: gb.ro.*
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- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
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- 32: em.htg.other.*
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- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	22	100.0	236	1	AF294958	AF294958 Unculture
C 2	22	100.0	260	1	AF389905	AF389905 Unculture
C 3	22	100.0	302	1	AY391637	AY391637 Unculture
C 4	22	100.0	302	1	AY391643	AY391643 Unculture
C 5	22	100.0	309	1	AY391670	AY391670 Unculture
C 6	22	100.0	368	6	AR071569	AR071569 Sequence
C 7	22	100.0	370	6	AR071568	AR071568 Sequence
C 8	22	100.0	372	1	AF257294	AF257294 Unculture
C 9	22	100.0	380	13	UMI241780	UMI241780 Unidentif
C 10	22	100.0	420	3	AF535201	AF535201 Unculture
C 11	22	100.0	431	1	AF226208	AF226208 Unculture
C 12	22	100.0	432	1	AY191889	AY191889 Unculture
C 13	22	100.0	458	1	AB041277	AB041277 Unculture
C 14	22	100.0	473	1	AF385928	AF385928 Mobiluncu
C 15	22	100.0	497	1	AF289914	AF289914 Unculture
C 16	22	100.0	498	6	AR071534	AR071534 Sequence
C 17	22	100.0	499	1	AXXRG16SC	LO9057 Unknown ana
C 18	22	100.0	500	3	AY038517	AY038517 Unculture
C 19	22	100.0	510	1	AB075168	AB075168 Unculture
C 20	22	100.0	519	1	AY261423	AY261423 Unculture
C 21	22	100.0	527	1	AY090655	AY090655 Unculture
C 22	22	100.0	550	1	AF449786	AF449786 Unculture
C 23	22	100.0	562	1	AF027037	AF027037 Unidentif
C 24	22	100.0	584	13	UMI241721	UMI241721 Unidentif
C 25	22	100.0	600	1	AF332350	AF332350 Unculture
C 26	22	100.0	600	1	AF429144	AF429144 Unculture
C 27	22	100.0	600	1	AF429158	AF429158 Unculture
C 28	22	100.0	600	1	AF429234	AF429234 Unculture
C 29	22	100.0	604	1	AY012520S2	AY012521 Unidentif
C 30	22	100.0	626	1	AF027077	AF027077 Unidentif
C 31	22	100.0	633	1	AY235614	AY235614 Unculture
C 32	22	100.0	645	1	AF320943S2	AF320944 Unculture
C 33	22	100.0	655	1	AY217417	AY217417 Unculture
C 34	22	100.0	673	1	AF320967S2	AF320968 Unculture
C 35	22	100.0	681	1	AY235670	AY235670 Unculture
C 36	22	100.0	689	1	AY100537	AY100537 Unculture
C 37	22	100.0	695	1	AF422641	AF422641 Unculture
C 38	22	100.0	695	1	AF424241	AF424241 Unculture
C 39	22	100.0	699	1	AF422682	AF422682 Unculture
C 40	22	100.0	719	1	UB294006	Z94006 Unidentifie
C 41	22	100.0	739	1	AY133110	AY133110 Unculture
C 42	22	100.0	760	1	AF424258	AF424258 Unculture
C 43	22	100.0	760	1	AY239544	AY239544 Unculture
C 44	22	100.0	762	1	AF422623	AF422623 Unculture
C 45	22	100.0	781	1	AY239537	AY239537 Unculture

ALIGNMENTS

RESULT 1	AF294958/c	AF294958	236 bp	DNA	linear	BCT 10-JAN-2002
LOCUS	AF294958/c	Uncultured eubacterium OTU1 16S	ribosomal RNA gene, partial			
DEFINITION	AF294958	sequence.				
ACCESSION	AF294958					
VERSION	AF294958.1	GI:15419629				
KEYWORDS						
SOURCE		uncultured eubacterium				
ORGANISM		uncultured eubacterium				
REFERENCE		Bacteria; environmental				
AUTHORS		1 (bases 1 to 236)				
TITLE		Cutter,L.A., Watts,J.E., Sowers,K.R. and May,H.D.				
		Identification of a microorganism that links its growth to the				
		reductive dechlorination of 2,3,5,6-chlorobiphenyl				

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
Indications for acetate as the carbon source and electron donor in anaerobic ortho PCB dechlorination

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (11-AUG-2000) Center of Marine Biotechnology, 701 E. Pratt St., Baltimore, MD 21202, USA

FEATURES
source
Location/Qualifiers
1. .236
/organism="uncultured eubacterium"
/mol_type="genomic DNA"
/db_xref="taxon:73429"
/note="OTU 1; PCB dechlorinating culture"
<1. .>236
/product="16S ribosomal RNA"

rRNA
source

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Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGAACGTATTCA 22
Db 207 ACAAGGCCGAGAACGTATTCA 186

RESULT 2
LOCUS
DEFINITION
Uncultured green sulfur bacterium clone OTU 1 16S ribosomal RNA gene, partial sequence.
ACCESSION
AF389905
VERSION
AF389905.1 GI:18643063
KEYWORDS
uncultured Chlorobi bacterium
SOURCE
ORGANISM
Bacteria; Chlorobi; environmental samples.
REFERENCE
1 (bases 1 to 260)
Wu, Q., Watts, J.E., Sowers, K.R. and May, H.D.
TITLE
Identification of a bacterium that specifically catalyzes the reductive dechlorination of polychlorinated biphenyls with doubly flanked chlorines

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (11-JUN-2001) Center of Marine Biotechnology, University of Maryland Biotechnology Institute, Columbus Center, 701 E. Pratt St., Baltimore, MD 21202, USA

FEATURES
source
Location/Qualifiers
1. .260
/organism="uncultured Chlorobi bacterium"
/mol_type="genomic DNA"
/db_xref="taxon:156405"
/clone="OTU 1"
/note="DNA sequence from PCB-dechlorinating enrichment culture"
<1. .>260
/product="16S ribosomal RNA"

rRNA
source

ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGAACGTATTCA 22
Db 207 ACAAGGCCGAGAACGTATTCA 186

RESULT 3
LOCUS
DEFINITION
Uncultured soil bacterium clone M21 16S ribosomal RNA gene, partial sequence.
ACCESSION
AY391637
VERSION
AY391637.1 GI:37624038
KEYWORDS
uncultured soil bacterium
SOURCE
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 (bases 1 to 302)
Sun, H., Deng, S. and Raun, W.R.
TITLE
Microbiology community structure and diversity in a century-long manure-treated agroecosystem
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 302)
Sun, H., Deng, S. and Raun, W.R.
TITLE
Direct Submission
JOURNAL
Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA

FEATURES
source
Location/Qualifiers
1. .302
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
/isolation_source="total microbial community of century-long manure-treated soil"
/db_xref="taxon:164851"
/clone="M21"
/environmental_sample
<1. .>302
/product="16S ribosomal RNA"

rRNA
source

ORIGIN
Query Match 100.0%; Score 22; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCGAGAACGTATTCA 22
Db 289 ACAAGGCCGAGAACGTATTCA 268

RESULT 4
LOCUS
DEFINITION
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ACCESSION
AY391643
VERSION
AY391643.1 GI:37624044
KEYWORDS
uncultured soil bacterium
SOURCE
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 (bases 1 to 302)
Sun, H., Deng, S. and Raun, W.R.
TITLE
Microbiology community structure and diversity in a century-long manure-treated agroecosystem
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 302)
Sun, H., Deng, S. and Raun, W.R.
TITLE
Direct Submission
JOURNAL
Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA

FEATURES
source
Location/Qualifiers
1. .302
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"

/isolation_source="total microbial community of century-long manure-treated soil"
/db_xref="taxon:164851"
/clone="M27"
/environmental_sample
<1..>302
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTAATCA 22
|||||
Db 289 ACAAGGCCCGAGAACGTAATCA 268
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RESULT 5
AY391670/c
LOCUS
DEFINITION
Accession
Version
Source
Keywords
Organism
Reference
Authors
Title
Journal
Features

AY391670 309 bp DNA linear BCT 15-OCT-2003
Uncultured soil bacterium clone M54 16S ribosomal RNA gene, partial sequence.
AY391670
AY391670.1 GI:37624071
uncultured soil bacterium
Bacteria; environmental samples.
1 (bases 1 to 309)
Sun, H., Deng, S. and Raun, W.R.
Microbiology community structure and diversity in a century-long manure-treated agroecosystem
Unpublished
2 (bases 1 to 309)
Sun, H., Deng, S. and Raun, W.R.
Direct Submission
Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State University, 368 Ag Hall, Stillwater, OK 74078, USA
Location/Qualifiers
1..309
/organism="uncultured soil bacterium"
/mol_type="genomic DNA"
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/db_xref="taxon:164851"
/clone="M54"
/environmental_sample
<1..>309
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTAATCA 22
|||||
Db 296 ACAAGGCCCGAGAACGTAATCA 275
|||||

RESULT 6
AR071569/c
LOCUS
DEFINITION
Accession
Version
Source
Keywords
Organism
Reference
Authors

AR071569 368 bp DNA linear PAT 18-FEB-2000
Sequence 36 from patent US 5912117.
AR071569
AR071569.1 GI:7222457
Unknown.
Unclassified.
1 (bases 1 to 368)
Dodge, D.E. and White, T.J.

TITLE Method for diagnosis of Lyme disease
JOURNAL Patent: US 5912117-A 35 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..368
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTAATCA 22
|||||
Db 273 ACAAGGCCCGAGAACGTAATCA 252
|||||

RESULT 7
AR071568/c
LOCUS
DEFINITION
Accession
Version
Source
Keywords
Organism
Reference
Authors
Title
Journal
Features

AR071568 370 bp DNA linear PAT 18-FEB-2000
Sequence 35 from patent US 5912117.
AR071568
AR071568.1 GI:7222456
Unknown.
Unclassified.
1 (bases 1 to 370)
Dodge, D.E. and White, T.J.
Method for diagnosis of Lyme disease
Patent: US 5912117-A 35 15-JUN-1999;
Location/Qualifiers
1..370
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCCCGAGAACGTAATCA 22
|||||
Db 275 ACAAGGCCCGAGAACGTAATCA 254
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RESULT 8
AF257294/c
LOCUS
DEFINITION
Accession
Version
Source
Keywords
Organism
Reference
Authors
Title
Journal
Features

AF257294 372 bp DNA linear BCT 09-JUL-2001
Uncultured marine gamma proteobacterium DHB-31 16S ribosomal RNA gene, partial sequence.
AF257294
AF257294.1 GI:14317937
uncultured marine gamma proteobacterium DHB-31
uncultured marine gamma proteobacterium DHB-31
Bacteria; Proteobacteria; Gammaproteobacteria; environmental samples.
1 (bases 1 to 372)
Lopez-Garcia, P., Lopez-Lopez, A., Moreira, D. and Rodriguez-Valera, F.
Diversity of free-living prokaryotes from a deep-sea site at the Antarctic Polar Front
FEMS Microbiol. Ecol. 36 (2-3), 193-202 (2001)
11451524
2 (bases 1 to 372)
Lopez-Garcia, P., Lopez-Lopez, A., Moreira, D. and Rodriguez-Valera, F.
Direct Submission
Submitted (18-APR-2000) Microbiology, University Miguel Hernandez, Facultad de Medicina, Campus de San Juan, San Juan, Alicante 03550, Spain
Location/Qualifiers
1..372
/organism="uncultured marine gamma proteobacterium DHB-31"


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RESULT 12
AY191889/c
LOCUS      432 bp      DNA      linear      BCT 10-MAR-2003
DEFINITION      Uncultured bacterium clone.BG6 16S ribosomal RNA gene, partial
sequence.
ACCESSION      AY191889
VERSION        AY191889.1  GI:28396218
KEYWORDS
SOURCE
ORGANISM      uncultured bacterium
Bacteria; environmental samples.
REFERENCE      1 (bases 1 to 432)
Macur,R.E., Langner,H.W. and Inskeep,W.P.
AUTHORS      Molecular analysis of microbial communities in
acid-sulfate-chloride-arsenic geothermal springs in Yellowstone
NATIONAL PARK
TITLE
JOURNAL
PUBLISHED
REFERENCE      2 (bases 1 to 432)
Macur,R.E., Langner,H.W. and Inskeep,W.P.
AUTHORS      Direct Submission
TITLE      Submitted (06-DEC-2002) Land Resources and Environmental Sciences,
JOURNAL      Montana State University - Bozeman, Leon Johnson Hall, Bozeman, MT
59717, USA
FEATURES
source
Location/Qualifiers
1..432
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="acid-sulfate-chloride-arsenic
geothermal spring"
/db_xref="taxon:77133"
/clone="BG6"
/environmental_sample
/country="USA; Wyoming, Yellowstone National Park"
<1..>432
/product="16S ribosomal RNA"

rRNA

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Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAAGGCCCGAGAACGTATTCA 22
|||||
Db      419  ACAAGGCCCGAGAACGTATTCA 398

RESULT 13
AB041277/c
LOCUS      458 bp      DNA      linear      BCT 29-NOV-2002
DEFINITION      Uncultured bacterium ECS7 gene for 16S ribosomal RNA, partial
sequence.
ACCESSION      AB041277.1  GI:10716064
VERSION        AB041277.1
KEYWORDS
SOURCE
ORGANISM      uncultured bacterium ECS7
Bacteria; environmental samples.
REFERENCE      1
AUTHORS      Sekiguchi,H., Koshikawa,H., Hiroki,M., Murakami,S., Xu,K.,
Watanabe,M., Nakahara,I., Zhu,M. and Uchiyama,H.
TITLE      Bacterial distribution and phylogenetic diversity in the Changjiang
estuary before the construction of the Three Gorges Dam
JOURNAL      Microb. Ecol. 43 (1), 82-91 (2002)
MEDLINE      22088774
PUBLISHED      11984631
REFERENCE      2 (bases 1 to 458)
Sekiguchi,H. and Uchiyama,H.
AUTHORS      Direct Submission
TITLE      Submitted (05-APR-2000) Hiroyuki Sekiguchi, National Institute for
Environmental Studies, Water Environment Quality; Onogawa16-2,
Tsukuba, Ibaraki 305-0053, Japan (E-mail:seki@nies.go.jp,
Tel:81-298-50-2412, Fax:81-298-50-2576)

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FEATURES
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/mol_type="genomic DNA"
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/clone="ECS7"
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/product="16S ribosomal RNA"

rRNA

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Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAAGGCCCGAGAACGTATTCA 22
|||||
Db      360  ACAAGGCCCGAGAACGTATTCA 339

RESULT 14
AF385928/c
LOCUS      473 bp      DNA      linear      BCT 02-JAN-2003
DEFINITION      Mobiluncus mulieris 16S-23S ribosomal RNA intergenic spacer,
partial sequence.
ACCESSION      AF385928
VERSION        AF385928.1  GI:27462290
KEYWORDS
SOURCE
ORGANISM      Mobiluncus mulieris
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Actinomycineae; Actinomycetaceae; Mobiluncus.
REFERENCE      1 (bases 1 to 473)
Park,H., Kim,C., Choi,H., Jang,H. and Kim,H.
AUTHORS      Mobiluncus curtisii DNA for 16S-23S rRNA internal transcribed
spacer
TITLE
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 473)
Park,H., Kim,C., Choi,H., Jang,H. and Kim,H.
AUTHORS      Direct Submission
TITLE      Submitted (25-MAY-2001) SJ Hightech Co., Ltd., College of Medicine,
JOURNAL      Pusan National University, 10 Amidong-1-Ga, Seogu, Pusan 602-739,
Korea
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="ATCC35243"
/db_xref="ATCC:35243"
/db_xref="taxon:2052"
<1..>473
/product="16S-23S ribosomal RNA intergenic spacer"

misc_RNA

ORIGIN
Query Match      100.0%; Score 22; DB 1; Length 473;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ACAAGGCCCGAGAACGTATTCA 22
|||||
Db      33  ACAAGGCCCGAGAACGTATTCA 12

RESULT 15
AF289914/c
LOCUS      497 bp      DNA      linear      BCT 09-APR-2001
DEFINITION      Uncultured green nonsulfur bacterium Kmlps6-20 16S ribosomal RNA
gene, partial sequence.
ACCESSION      AF289914
VERSION        AF289914.1  GI:9937457
KEYWORDS
SOURCE
ORGANISM      uncultured green non-sulfur bacterium Kmlps6-20
uncultured green non-sulfur bacterium Kmlps6-20
Bacteria; Chloroflexi; environmental samples.

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REFERENCE 1 (bases 1 to 488)
 AUTHORS Yu, Z. and Mohn, W. W.
 TITLE Bacterial diversity and community structure in an aerated lagoon revealed by ribosomal intergenic spacer analyses and 16S ribosomal DNA sequencing. Microbiol. 67 (4), 1565-1574 (2001)
 JOURNAL Appl. Environ. Microbiol. 67 (4), 1565-1574 (2001)
 MEDLINE 21178505
 PUBMED 11282606

REFERENCE 2 (bases 1 to 497)
 AUTHORS Yu, Z. and Mohn, W. W.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-2000) Microbiology and Immunology, University of British Columbia, #300-6174 University Blvd., Vancouver, BC V6T 1Z3, Canada

FEATURES
 source Location/Qualifiers
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 Kmlps6-20"
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 /clone="Kmlps6-20"
 <1..>497
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 100.0%; Score 22; DB 1; Length 497;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACAAGGCCCGAGACGTATTCA 22
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 Db 472 ACAAGGCCCGAGACGTATTCA 451

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 Job time : 965.229 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 875.663 Seconds
(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-2

Perfect score: 20

Sequence: 1 ggaggaagcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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9: gb.pr.*
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12: gb_sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
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23: em.ov.*
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36: em.htg_rod.*
37: em.htg_man.*
38: em.htg_vrt.*
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40: em.htgo.hum.*
41: em.htgo_mus.*
42: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	570	1	AB018671	AB018671 Endosymbi
2	20	100.0	601	1	AF507717	AF507717 Unculture
3	20	100.0	617	1	AY369151	AY369151 Unculture
4	20	100.0	827	1	AF317470	AF317470 Candidatu
5	20	100.0	857	1	AY220719	AY220719 Unculture
6	20	100.0	902	1	UBA309645	UBA309645 Unculture
7	20	100.0	910	1	UBA309647	UBA309647 Unculture
8	20	100.0	911	1	UBA309611	UBA309611 Unculture
9	20	100.0	936	1	AF050608	AF050608 Unculture
10	20	100.0	1247	1	UBA519648	UBA519648 Unculture
11	20	100.0	1255	1	AF524023	AF524023 Unculture
12	20	100.0	1298	1	APBRGDC	L35460 Alpha prote
13	20	100.0	1313	1	AB088955	AB088955 Unculture
14	20	100.0	1318	1	AF229791	AF229791 Unculture
15	20	100.0	1335	1	AF127027	AF127027 Helicobac
16	20	100.0	1354	1	CPU73782	U73782 Chlamydia p
17	20	100.0	1354	1	CPU73785	U73785 Chlamydia p
18	20	100.0	1355	1	CPU73783	U73783 Chlamydia p
19	20	100.0	1383	1	AY126640	AY126640 Endosymbi
20	20	100.0	1433	1	AY328728	AY328728 Unculture
21	20	100.0	1445	1	AF382129	AF382129 Unculture
22	20	100.0	1446	1	ME400342	ME400342 Unculture
23	20	100.0	1447	1	AF382141	AF382141 Unculture
24	20	100.0	1457	1	CP10L16SR	Z49874 C.pneumonia
25	20	100.0	1466	1	CPEA16SR	Z49871 Chlamydophi
26	20	100.0	1466	1	CPOA16SR	Z49872 Chlamydophi
27	20	100.0	1468	1	AF507685	AF507685 Unculture
28	20	100.0	1471	1	UAU75649	UAU75649 Unidentifi
29	20	100.0	1479	1	CFTW183RR	Z49873 C.pneumonia
30	20	100.0	1480	1	UEU408994	UEU408994 Unculture
31	20	100.0	1492	1	AY328720	AY328720 Unculture
32	20	100.0	1507	1	AB001778	AB001778 Chlamydo
33	20	100.0	1507	1	AB001779	AB001779 Chlamydo
34	20	100.0	1507	1	AB001780	AB001780 Chlamydo
35	20	100.0	1507	1	AB001781	AB001781 Chlamydo
36	20	100.0	1507	1	AB001782	AB001782 Chlamydo
37	20	100.0	1507	1	AB001783	AB001783 Chlamydo
38	20	100.0	1507	1	AB001784	AB001784 Chlamydo
39	20	100.0	1507	1	AB001785	AB001785 Chlamydo
40	20	100.0	1507	1	AB001786	AB001786 Chlamydo
41	20	100.0	1507	1	AB001787	AB001787 Chlamydo
42	20	100.0	1507	1	AB001788	AB001788 Chlamydo
43	20	100.0	1507	1	AB001789	AB001789 Chlamydo
44	20	100.0	1507	1	AB001790	AB001790 Chlamydo
45	20	100.0	1507	1	AB001791	AB001791 Chlamydo

ALIGNMENTS

RESULT 1
AB018671
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AB018671
Endosymbiont of *Camponotus kiusiuensis*
partial sequence.
AB018671
AB018671.1 GI:4587318
16S rRNA.
endosymbiont of *Camponotus kiusiuensis*
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
1 (sites)
Sameshima, S., Hasegawa, E., Kitade, O., Minaka, N. and Matsumoto, T.
Phylogenetic comparison of the endosymbionts with their host ants

570 bp DNA linear BCT 03-APR-1999
Endosymbiont of *Camponotus kiusiuensis* gene for 16S ribosomal RNA,
partial sequence.

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based on molecular evidences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 570)
AUTHORS Sameshima, S.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-1998) Shinya Sameshima, University of Tokyo,
Department of Biology, 3-8-1 Komaba, Meguro-ku, Tokyo 153-8902,
Japan (E-mail: ss77216hongo.ecc.u-tokyo.ac.jp, Tel: +81-3-5454-6652,
Fax: +81-3-5454-4322)
FEATURES
source
1..570
/organism="endosymbiont of Camponotus kiusiuenensis"
/mol_type="genomic DNA"
/db_xref="taxon:84570"
<1..570
/product="16S ribosomal RNA"

rRNA
ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20
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Db 355 GGAGGAGGCGGAGGATGACG 374

RESULT 2
AF507717 601 bp DNA linear BCT 03-JUN-2002
LOCUS Uncultured soil bacterium clone s13 16S ribosomal RNA gene, partial
DEFINITION
ACCESSION AF507717
VERSION AF507717.1 GI:20978172
KEYWORDS uncultured soil bacterium
SOURCE uncultured soil bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 601)
AUTHORS Dunbar, J., Barns, S.M., Ticknor, L.O. and Kuske, C.R.
TITLE Empirical and theoretical bacterial diversity in four Arizona soils
JOURNAL Appl. Environ. Microbiol. 68 (6), 3035-3045 (2002)
MEDLINE 22034980
PUBMED 12039765
REFERENCE 2 (bases 1 to 601)
AUTHORS Dunbar, J., Barns, S.M., Ticknor, L.O. and Kuske, C.R.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Biosciences Division, Los Alamos National
Laboratory, M888, Los Alamos, NM 87545, USA
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rRNA
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Best Local Similarity 100.0%; Pred. NO. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20
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Db 385 GGAGGAGGCGGAGGATGACG 404

RESULT 3
AY369151 617 bp DNA linear BCT 14-SEP-2003
LOCUS

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DEFINITION Uncultured bacterium clone F-OTU12 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY369151
VERSION AY369151.1 GI:34555665
KEYWORDS uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 617)
AUTHORS Zheng, X., Yang, H. and Li, D.
TITLE Analysis of the microbial community composition and transition in
the activated sludge of a lab-scale deammonification reactor by
molecular methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 617)
AUTHORS Zheng, X., Yang, H. and Li, D.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-2003) School of Life Science and Technology,
Shanghai Jiaotong University, No.800, Dongchuan Road, Shanghai
200240, China
FEATURES
source
1..617
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/db_xref="taxon:77133"
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rRNA
ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAGGCGGAGGATGACG 20
|||||
Db 252 GGAGGAGGCGGAGGATGACG 271

RESULT 4
AF317470 827 bp DNA linear BCT 04-FEB-2002
LOCUS Candidatus Helicobacter bovis strain Toro3A 16S ribosomal RNA gene,
partial sequence.
DEFINITION
ACCESSION AF317470
VERSION AF317470.1 GI:18482505
KEYWORDS Candidatus Helicobacter bovis
SOURCE Candidatus Helicobacter bovis
ORGANISM Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
REFERENCE 1 (bases 1 to 827)
AUTHORS Gueneau, P., Fuemmayor, J., Aristimuno, O.C., Cedeno, S., Baez, E.,
Reyes, N., Michelangeli, P. and Dominguez-Bello, M.G.
TITLE Are goats naturally resistant to gastric Helicobacter infection?
JOURNAL Vet. Microbiol. 84 (1-2), 115-121 (2002)
MEDLINE 21589087
PUBMED 11731164
REFERENCE 2 (bases 1 to 827)
AUTHORS Gueneau de Novoa, P.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-2000) CBB, IVIC, Km 11 Panamericana, Altos de
Pipe Miranda, Venezuela
FEATURES
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/strain="Toro3A"
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/note="sequence derived from a single PCR amplicon
obtained from the gastric mucosa of a bull from Venezuela"
<1..827

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ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 827;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGATGACG 20
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Db 713 GGAGGAAGCGGAGGATGACG 732

RESULT 5
LOCUS AY220719 857 bp DNA linear BCT 09-FEB-2003
DEFINITION Uncultured alpha proteobacterium clone WCPAP15 16S ribosomal RNA
gene, partial sequence.
ACCESSION AY220719
VERSION GI:28274894
KEYWORDS
SOURCE uncultured alpha proteobacterium
ORGANISM uncultured alpha proteobacterium
Bacteria; Proteobacteria; Alphaproteobacteria; environmental
samples.
REFERENCE 1 (bases 1 to 857)
AUTHORS Gallagher, J.M., Carton, M., Eardly, D.F. and Patching, J.W.
TITLE Prokaryotic community structure and biodiversity in deep waters of
the NE Atlantic
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 857)
AUTHORS Gallagher, J.M., Carton, M., Eardly, D.F. and Patching, J.W.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-2003) Microbiology, NUI, Galway, University Rd.,
Galway, Rep. of Ireland
FEATURES
source Location/Qualifiers
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Northeast Atlantic Ocean"
/db_xref="taxon:91750"
/clone="WCPAP15"
/environmental_sample
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/product="16S ribosomal RNA"

xRNA
Query Match 100.0%; Score 20; DB 1; Length 857;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGATGACG 20
| | | | | | | | | | | | | | | | | | | |
Db 641 GGAGGAAGCGGAGGATGACG 660

RESULT 6
LOCUS UBA309645 902 bp DNA linear BCT 06-JUN-2003
DEFINITION Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
P6-C03.
ACCESSION AJ309645
VERSION GI:15552891
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Chloroflexales bacterium
ORGANISM uncultured Chloroflexales bacterium
Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE 1 (bases 1 to 902)
AUTHORS Nubel, U., Bateson, M.M., Madigan, M.T., Kuhl, M. and Ward, D.M.
TITLE Diversity and distribution in hypersaline microbial mats of
bacteria related to Chloroflexus spp
JOURNAL Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
MEDLINE 21417071

ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 857;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGCGGAGGATGACG 20
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Db 641 GGAGGAAGCGGAGGATGACG 660

RESULT 6
LOCUS UBA309645 902 bp DNA linear BCT 06-JUN-2003
DEFINITION Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
P6-C03.
ACCESSION AJ309645
VERSION GI:15552891
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Chloroflexales bacterium
ORGANISM uncultured Chloroflexales bacterium
Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE 1 (bases 1 to 902)
AUTHORS Nubel, U., Bateson, M.M., Madigan, M.T., Kuhl, M. and Ward, D.M.
TITLE Diversity and distribution in hypersaline microbial mats of
bacteria related to Chloroflexus spp
JOURNAL Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
MEDLINE 21417071

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Db      780 GGAGGAAGCGGAGGATGACG 799
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RESULT 8
UBA309611      911 bp      DNA      linear      BCT 06-JUN-2003
DEFINITION    Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
               P4-D01.
ACCESSION     AJ309611      GI:15552857
VERSION       16S ribosomal RNA; 16S rRNA gene.
KEYWORDS      uncultured Chloroflexales bacterium
SOURCE        uncultured Chloroflexales bacterium
ORGANISM      Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE     1 (bases 1 to 911)
AUTHORS       Nubel,U., Bateson,M.M., Madigan,M.T., Kuhl,M. and Ward,D.M.
TITLE         Diversity and distribution in hypersaline microbial mats of
               bacteria related to Chloroflexus spp
JOURNAL       Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
MEDLINE       21417071
PUBMED        11526049
REFERENCE     2 (bases 1 to 911)
AUTHORS       Nubel,U.
TITLE         Direct Submission
JOURNAL       Submitted (09-FEB-2001) Nubel U., Molekulare Systematik und
               Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
               Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
FEATURES     source
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               /db_xref="taxon:152575"
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               1. .911
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gene
rRNA

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Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGAAGCGGAGGATGACG 20
|||||
Db      781 GGAGGAAGCGGAGGATGACG 800
|||||

RESULT 9
AF050608      936 bp      DNA      linear      BCT 15-OCT-1998
LOCUS         Uncultured eubacterium WCHAL-16
DEFINITION    Uncultured eubacterium WCHAL-16 16S ribosomal RNA gene, partial
               sequence.
ACCESSION     AF050608      1 GI:2967784
VERSION       uncultured eubacterium WCHAL-16
KEYWORDS      Bacteria; candidate division OP11; environmental samples.
SOURCE        uncultured eubacterium WCHAL-16
ORGANISM      Bacteria; candidate division OP11; environmental samples.
REFERENCE     1 (bases 1 to 936)
AUTHORS       Dojka,M.A., Hugenholtz,P., Haack,S.K. and Pace,N.R.
TITLE         Microbial diversity in a hydrocarbon- and
               chlorinated-solvent-contaminated aquifer undergoing intrinsic
               bioremediation
JOURNAL       Appl. Environ. Microbiol. 64 (10), 3869-3877 (1998)
MEDLINE       98432811
PUBMED        9758812
REFERENCE     2 (bases 1 to 936)
AUTHORS       Dojka,M.A. Jr., Hugenholtz,P., Haack,S. and Pace,N.R.
TITLE         Direct Submission

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JOURNAL       Submitted (24-FEB-1998) Plant and Microbial Biology, University of
               California, Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA
FEATURES     source
               1. .936
               /organism="uncultured eubacterium WCHAL-16"
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               /db_xref="taxon:74258"
               /clone="WCHAL-16"
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rRNA

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGAAGCGGAGGATGACG 20
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Db      629 GGAGGAAGCGGAGGATGACG 648
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RESULT 10
UBA519648      1247 bp      rRNA      linear      BCT 29-NOV-2002
LOCUS         Uncultured bacterium partial 16S rRNA gene, clone Sh765B-AG-14.
DEFINITION    Uncultured bacterium partial 16S rRNA gene, clone Sh765B-AG-14.
ACCESSION     AJ519648
VERSION       16S ribosomal RNA; 16S rRNA gene.
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE        uncultured bacterium
ORGANISM      Bacteria; environmental samples.
REFERENCE     1 Geissler,A.
               Bakterielle Diversitaet in Erdproben aus Uranabfallhalden
TITLE         Unpublished
JOURNAL       Unpublished
AUTHORS       Geissler,A., Tzvetkova,T., Flemming,K. and Selsenska-Pobell,S.
TITLE         Comparison of natural bacterial communities found in uranium mining
               waste piles and mill tailings
JOURNAL       Unpublished
REFERENCE     3 (bases 1 to 1247)
AUTHORS       Selsenska-Pobell,S.I.
TITLE         Direct Submission
JOURNAL       Submitted (28-NOV-2002) Selsenska-Pobell S.I., Molecular
               Microbiology, Institute of Radiochemistry, FZK, P.O.B. 51 01 19,
               D-01314 Dresden, GERMANY
FEATURES     Location/Qualifiers
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               /clone="Sh765B-AG-14"
               /clone_lib="43F-1404R"
               /environmental_sample
               /country="USA:Shiprock, New Mexico"
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gene
rRNA

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 1247;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAGGAAGCGGAGGATGACG 20
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Db      1048 GGAGGAAGCGGAGGATGACG 1067
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RESULT 11
AF524023
LOCUS      AF524023      1255 bp      DNA      linear      BCT 26-DEC-2002
DEFINITION Uncultured bacterium clone FW128 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  AF524023
VERSION    AF524023.1  GI:21952426
KEYWORDS   uncultured bacterium
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE  1 (bases 1 to 1255)
AUTHORS   Brofft,J.E., Shinkets,L.J. and McArthur,J.V.
TITLE     Recovery of novel bacterial diversity from a forested wetland
          impacted by reject coal
JOURNAL   Environ. Microbiol. 4 (11), 764-769 (2002)
MEDLINE   22349383
PUBMED    12460285

REFERENCE  2 (bases 1 to 1255)
AUTHORS   Brofft,J.E., Shinkets,L.J. and McArthur,J.V.
TITLE     Direct Submission
JOURNAL   Submitted (24-JUN-2002) Microbiology, University of Georgia, 527
          Biological Sciences, Athens, GA 30602, USA

FEATURES   Location/Qualifiers
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                /clone="FW128"
                /environmental_sample
              <1..>1255
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      100.0%;      Score 20;      DB 1;      Length 1255;
Best Local Similarity 100.0%;      Pred. No. 32;
Matches 20;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

QY  1  GGAGGAGGCGGAGGATGACG 20
      |||||
Db   1076 GGAGGAGGCGGAGGATGACG 1095

RESULT 12
APBRGDC
LOCUS      APBRGDC      1298 bp      DNA      linear      BCT 13-SEP-2002
DEFINITION Alpha proteobacterium sp. (clone SAR102) 16S ribosomal RNA (16S
            rRNA) gene, complete rRNA.
ACCESSION  L35460
VERSION    L35460.1  GI:529971
KEYWORDS   16S ribosomal RNA.
SOURCE     uncultured alpha proteobacterium
ORGANISM   Bacteria; Proteobacteria; Alphaproteobacteria; environmental
            samples.

REFERENCE  1 (bases 1 to 1298)
AUTHORS   Mullins,T.D., Britschgi,T.B., Krest,R.L. and Giovannoni,S.J.
TITLE     Genetic comparisons reveal the same unknown bacterial lineages in
          Atlantic and Pacific Bacterioplankton communities
JOURNAL   Limnol. Oceanogr. 40 (1), 147-158 (1995)
COMMENT   Original source text: Alpha proteobacterium sp (clone: SAR102) DNA.
FEATURES   Location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:91750"
                /clone="SAR102"
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gene

rRNA

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ORIGIN
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Best Local Similarity 100.0%;      Pred. No. 32;
Matches 20;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

QY  1  GGAGGAGGCGGAGGATGACG 20
      |||||
Db   1067 GGAGGAGGCGGAGGATGACG 1086

RESULT 13
AB088955
LOCUS      AB088955      1313 bp      DNA      linear      BCT 26-APR-2003
DEFINITION Uncultured Eubacteriaceae bacterium gene for 16S rRNA, partial
            sequence, clone:Rs-M13.
ACCESSION  AB088955
VERSION    AB088955.1  GI:27530167
KEYWORDS   uncultured Eubacteriaceae bacterium
SOURCE     uncultured Eubacteriaceae bacterium
ORGANISM   Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
            environmental samples.

REFERENCE  1
AUTHORS   Hongoh,Y., Ohkuma,M. and Kudo,T.
TITLE     Molecular analysis of bacterial microbiota in the gut of the
          termite Reticulitermes speratus (Isoptera; Rhinotermitidae)
JOURNAL   FEMS Microbiol. Ecol. 44, 231-242 (2003)
REFERENCE  2 (bases 1 to 1313)
AUTHORS   Hongoh,Y., Ohkuma,M. and Kudo,T.
TITLE     Direct Submission
JOURNAL   Submitted (26-JUL-2002) Yuichi Hongoh, Japan Science and Technology
          Corporation (JST), Bio-Recycle Project, International Cooperative
          Research Project; Hiroseawa 2-1, Wako-shi, Saitama 351-0198, Japan
          (E-mail:yhongoh@postman.riken.go.jp, Tel:81-48-467-9546,
          Fax:81-48-462-4672)
FEATURES   Location/Qualifiers
            source
              1..1313
                /organism="uncultured Eubacteriaceae bacterium"
                /mol_type="genomic DNA"
                /isolation_source="PCR-derived sequence from termite gut
                  homogenate"
                /specific_host="Reticulitermes speratus"
                /db_xref="taxon:203524"
                /clone="Rs-M13"
                /environmental_sample
                /country="Japan:Saitama, Ogose"
                <1..>1313
                /product="16S ribosomal RNA"

rRNA

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Query Match      100.0%;      Score 20;      DB 1;      Length 1313;
Best Local Similarity 100.0%;      Pred. No. 32;
Matches 20;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

QY  1  GGAGGAGGCGGAGGATGACG 20
      |||||
Db   1099 GGAGGAGGCGGAGGATGACG 1118

RESULT 14
AF229791
LOCUS      AF229791      1318 bp      DNA      linear      BCT 01-FEB-2001
DEFINITION Uncultured bacterium TA18 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF229791
VERSION    AF229791.1  GI:12642398
KEYWORDS   uncultured bacterium TA18
SOURCE     uncultured bacterium TA18
ORGANISM   Bacteria; environmental samples.

REFERENCE  1 (bases 1 to 1318)
AUTHORS   Wu,J.H., Liu,W.T., Tseng,I.C. and Cheng,S.S.
TITLE     Characterization of microbial consortia in a

```

terephthalate-degrading anaerobic granular sludge system
Microbiology 147 (Pt 2), 373-382 (2001)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1318)
Wu, J.H., Liu, W.T., Tseng, I.C. and Cheng, S.S.
Direct Submission

Submitted (01-FEB-2000) Department of Environmental Engineering,
National Cheng Kung University, 1 University Road, Tainan 701,
Taiwan, ROC

FEATURES

Location/Qualifiers

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/organism="uncultured bacterium TA18"
/mol_type="genomic DNA"
/db_xref="taxon:150044"
/clone="TA18"
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/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 1318;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGAGGAAGCGGAGGATGACG 20

Db 1026 GGAGGAAGCGGAGGATGACG 1045

RESULT 15

AF127027

LOCUS

AF127027 1335 bp DNA linear BCT 17-NOV-1999
Helicobacter bovis 16S ribosomal RNA gene, partial sequence.

DEFINITION

AF127027

ACCESSION

AF127027.1 GI:6018194

VERSION

KEYWORDS

SOURCE

ORGANISM

Candidatus Helicobacter bovis
Candidatus Helicobacter bovis
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
1 (bases 1 to 1335)
De Groot, D., van Doorn, L.J., Ducatelle, R., Verschuren, A.,
Tilmant, K., Quint, W.G., Haesebrouck, F., Quint, W. and Vandamme, P.
Phylogenetic characterization of 'Candidatus Helicobacter bovis', a
new gastric helicobacter in cattle

Int. J. Syst. Bacteriol. 49 Pt 4, 1707-1715 (1999)

20023052

MEDLINE

PUBMED

REFERENCE

AUTHORS

De Groot, D., van Doorn, L.-J., Ducatelle, R., Verschuren, A.,
Tilmant, K., Haesebrouck, F., Quint, W. and Vandamme, P.

Direct Submission

TITLE

Submitted (09-FEB-1999) Pathology, Bacteriology and Avian Diseases,
University Ghent, Salisburylaan 133, Merelbeke B-9820, Belgium

JOURNAL

FEATURES

source

1..1335
/organism="Candidatus Helicobacter bovis"
/mol_type="genomic DNA"
/specific_host="Bos taurus"
/db_xref="taxon:104629"
/clone="R2XA"
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rRNA

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGAGGAAGCGGAGGATGACG 20

Db 1103 GGAGGAAGCGGAGGATGACG 1122

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GenCore version 5.1.6
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Gapop_50.0, Gapext 50.0

Searched: 3470272 seqs, 21671516995 residues
Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	23	6	AX575427	AX575427 Sequence
2	20	100.0	37	6	AX709025	AX709025 Sequence
3	20	100.0	47	6	BD140316	BD140316 Universal
4	20	100.0	129	1	MCO16SR2	D11230 Marinomonas
5	20	100.0	131	1	LPNRDA02	M19442 L.pneumophi
6	20	100.0	131	1	TAMRDB01	M19451 T.micdadei
7	20	100.0	131	1	TAMRDB02	M19446 T.micdadei
8	20	100.0	131	1	VIB16SR11	D11247 Vibrio chol
9	20	100.0	133	1	TAMRDBA02	M19449 T.micdadei
10	20	100.0	137	1	CLO16SRNA	M98449 Clostridium
11	20	100.0	137	1	LPNRDC02	M19444 L.pneumophi
12	20	100.0	137	6	E05154	Sequence of
13	20	100.0	138	1	CLODNA16S	L08598 Clostridium
14	20	100.0	140	1	LPNMRNO2	M24643 F.bozemanae
15	20	100.0	140	1	LPNDRRNO2	M24642 F.dumoffii
16	20	100.0	150	1	ALTE16SR2	D11220 Alteromonas
17	20	100.0	150	1	VIB16SR12	D11248 Vibrio chol
18	20	100.0	155	1	AEOS16SR	D11224 Aeromonas s
19	20	100.0	161	6	E05163	Sequence of
20	20	100.0	164	1	TAMRNO2	M34713 T.maceacher
21	20	100.0	176	1	D28568S2	D28569 Sphingomona
22	20	100.0	176	1	D28571S2	D28572 Sphingomona
23	20	100.0	176	1	D28574S2	D28575 Sphingomona
24	20	100.0	176	1	VIB16SR10	D11246 Vibrio chol
25	20	100.0	178	1	PHRL16SR	D11233 Photobacter
26	20	100.0	182	1	AECH16SR2	D11219 Aeromonas h
27	20	100.0	183	1	UOU46521	U46521 Unidentifie
28	20	100.0	188	1	AY373834	AY373834 Unculture
29	20	100.0	189	1	AY373835	AY373835 Unculture
30	20	100.0	191	1	VIB16SR20	D11256 Vibrio loge
31	20	100.0	191	6	AX575429	AX575429 Sequence
32	20	100.0	192	1	AF045813	AF045813 Unculture
33	20	100.0	193	1	AF228141	AF228141 Marine se
34	20	100.0	193	1	AF228146	AF228146 Marine se
35	20	100.0	195	6	I28355	I28355 Sequence 7
36	20	100.0	195	6	BD011645	BD011645 DNA oligo
37	20	100.0	196	1	AF045815	AF045815 Unculture
38	20	100.0	200	1	AF045823	AF045823 Unculture
39	20	100.0	200	1	UBA421167	AJ421167 Unculture
40	20	100.0	200	1	UEU405022	AJ405022 unculture
41	20	100.0	203	1	AF045827	AF045827 Unculture
42	20	100.0	206	1	ALTH16SR2	D11221 Alteromonas
43	20	100.0	207	1	AEOM16SR	D11223 Aeromonas m
44	20	100.0	207	1	LAEP16SR2	D11229 Listonella
45	20	100.0	207	1	VIB16SR13	D11249 Vibrio cost

ALIGNMENTS

RESULT 1
AX575427
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX575427
Sequence 2 from Patent WO02077271.
AX575427
AX575427.1 GI:27552061
synthetic construct
synthetic construct
artificial sequences.
1
Vollenbroich,D. and Schramm,C.
Control plasmid and method for detecting mycoplasma contamination
in biological material
Patent: WO 02077271-A 2 03-OCT-2002;

23 bp
DNA
linear
PAT 07-JAN-2003

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  source
    Minerva Biolabs GmbH (DE)
    Location/Qualifiers
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      /db_xref="taxon:32630"
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  Best Local Similarity 100.0%; Pred. No. 1.6e+05;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACGAGGATTAGATACCC 20
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Db 4 GCAACACGAGGATTAGATACCC 23

RESULT 2
AX709025          AX709025          37 bp      DNA      linear      PAT 04-APR-2003
DEFINITION      Sequence 1 from Patent WO03014382.
ACCESSION      AX709025
VERSION        AX709025.1 GI:29564699
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE 1
AUTHORS        Mittermayr,C.R., Ronacher,B., Wanner,F. and Zehethofer,K.
TITLE          Device for analyzing nucleic acid
JOURNAL        Patent: WO 03014382-A 1 20-FEB-2003;
              Lambda Labor fuer Molekularbiologische DNA-Analysen GmbH (AT)
FEATURES
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RESULT 3
BD140316/c
LOCUS            BD140316            47 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION      Universal eubacteria nucleic acid probe and method.
ACCESSION      BD140316
VERSION        BD140316.1 GI:23235261
KEYWORDS        JP 2002051799-A/9.
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE 1 (bases 1 to 47)
AUTHORS        Lane,D.J., Shah,J., Buharin,A. and Weisburg,W.G.
TITLE          Universal eubacteria nucleic acid probe and method
JOURNAL        Patent: JP 2002051799-A 9 19-FEB-2002;
              GENE TRAK SYSTEMS
COMMENT         OS Artificial Sequence
              PN JP 2002051799-A/9
              PD 19-FEB-2002
              PF 11-APR-2001 JP 2001150160
              PR 31-MAY-1989 US 359158
              PI DAVID J. LANE,JYOTSNA SHAH,AMELIA BUHARIN,WILLIAM G WEISBURG PC
              C12Q1/68,C12N15/09,C12N15/09,C12N15/00,C12N15/00 CC Synthesized
              probe for hybridization

FEATURES
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    Location/Qualifiers
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  Query Match      100.0%; Score 20; DB 1; Length 129;
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACGAGGATTAGATACCC 20
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Db 4 GCAACACGAGGATTAGATACCC 23

RESULT 5
LPNRRDA02
LOCUS            LPNRRDA02            131 bp      rRNA      linear      BCT 23-JUL-1993
DEFINITION      L.pneumophila (strain Chicago-2) 16S rRNA, partial, segment 2 of 3.
ACCESSION      M19442
VERSION        M19442.1 GI:175170
KEYWORDS        16S ribosomal RNA.
SOURCE          2 of 3
              Legionella pneumophila
              ORGANISM Legionella pneumophila
              Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

FEATURES
  source
    Location/Qualifiers
      1..129
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Qy 1 GCAACACGAGGATTAGATACCC 20
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Db 4 GCAACACGAGGATTAGATACCC 23

RESULT 4
MC016SR2
LOCUS            MC016SR2            129 bp      rRNA      linear      BCT 04-NOV-1999
DEFINITION      Marinomonas communis 16S rRNA.
ACCESSION      D11230
VERSION        D11230.1 GI:286047
KEYWORDS        Marinomonas communis
SOURCE          Marinomonas communis
ORGANISM        Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
              Marinomonas.
REFERENCE 1 (bases 1 to 129)
AUTHORS        Kita-Tsukamoto,K., Oyaizu,H., Namba,K. and Simidu,U.
TITLE          Phylogenetic relationships of marine bacteria, mainly members of
              the family Vibrionaceae, determined on the basis of 16S rRNA
              sequences
JOURNAL        Int. J. Syst. Bacteriol. 43 (1), 8-19 (1993)
MEDLINE        93152464
PUBMED        8427811
REFERENCE 2 (bases 1 to 129)
AUTHORS        Kita-Tsukamoto,K.
TITLE          Direct Submission
JOURNAL        Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
              Ocean Research Institute; 1-15-1 Minamidai, Nakano-Ku, Tokyo 164,
              Japan (E-mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
              Fax:03-3375-6716)
FEATURES
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    Location/Qualifiers
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ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 6e+04;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACACGAGGATTAGATACCC 20
    |||||
Db 4 GCAACACGAGGATTAGATACCC 23

RESULT 5
LPNRRDA02
LOCUS            LPNRRDA02            131 bp      rRNA      linear      BCT 23-JUL-1993
DEFINITION      L.pneumophila (strain Chicago-2) 16S rRNA, partial, segment 2 of 3.
ACCESSION      M19442
VERSION        M19442.1 GI:175170
KEYWORDS        16S ribosomal RNA.
SOURCE          2 of 3
              Legionella pneumophila
              ORGANISM Legionella pneumophila
              Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/organism="Legionella pneumophila"
/mol_type="rRNA"
/db_xref="taxon:446"
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/product="16S ribosomal RNA"
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Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
|||||
Db 4 GCAACAGGATTAGATACCC 23

RESULT 6
TAMRD01
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .131
/organism="Tatlockia micdadei"
/mol_type="rRNA"
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<1..>131
/product="16S ribosomal RNA"
About 250 bp after segment 1.
Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
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Db 4 GCAACAGGATTAGATACCC 23

RESULT 7
TAMRD02
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .131
/organism="Tatlockia micdadei"
/mol_type="rRNA"
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About 250 bp after segment 1.
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Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
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Db 4 GCAACAGGATTAGATACCC 23

RESULT 8
VIB16SR11
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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About 250 bp after segment 1.
Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
|||||
Db 4 GCAACAGGATTAGATACCC 23

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RESULT 7
TAMRD02
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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/organism="Tatlockia micdadei"
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/db_xref="taxon:451"
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/product="16S ribosomal RNA"
About 250 bp after segment 1.
Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
|||||
Db 4 GCAACAGGATTAGATACCC 23

RESULT 8
VIB16SR11
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="Vibrio cholerae"
/mol_type="rRNA"
/db_xref="taxon:451"
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/product="16S ribosomal RNA"
About 250 bp after segment 1.
Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
|||||
Db 4 GCAACAGGATTAGATACCC 23

RESULT 9
VIB16SR11
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="Vibrio cholerae"
/mol_type="rRNA"
/db_xref="taxon:451"
<1..>131
/product="16S ribosomal RNA"
About 250 bp after segment 1.
Query Match 100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
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Db 4 GCAACAGGATTAGATACCC 23

```



```

LOCUS      E05154      137 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Sequence of a DNA fraction prepared by a restriction enzyme HAP II
            from DNA coding for E.coli 16S ribosome RNA.
ACCESSION  E05154
VERSION    E05154.1 GI:2173347
KEYWORDS   JP 1993192147-A/26.
SOURCE     Escherichia coli
ORGANISM   Escherichia coli
REFERENCE  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AUTHORS    Enterobacteriaceae; Escherichia.
TITLE      Shitazu.Y.
JOURNAL    METHOD FOR SPECIFYING DNA BASE SEQUENCE
COMMENT    Patent: JP 1993192147-A 26 03-AUG-1993;
          KIRIN BIBARETSUJI KK
          OS Escherichia coli
          PN JP 1993192147-A/26
          PD 03-AUG-1993
          PF 15-NOV-1991 JP 1991300882
          PI SHIRASU YOSHITARU
          PC C12N15/00,C12Q1/06,C12Q1/68;
          CC strandedness: Doublet;
          CC topology: Linear;
          CC *source: strain-K12.
FEATURES   Location/Qualifiers
            source
              1..137
              /organism="Escherichia coli"
              /mol_type="genomic DNA"
              /db_xref="taxon:562"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
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Db 58 GCAACAGGATTAGATACCC 77

RESULT 13
LOCUS      CLORDNA16S      138 bp      DNA      linear      BCT 28-MAR-1994
DEFINITION Clostridium butyricum 16S ribosomal DNA gene.
ACCESSION  L08598
VERSION    L08598.1 GI:144899
KEYWORDS   16S ribosomal DNA.
SOURCE     Clostridium butyricum
ORGANISM   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE  1 (sites)
AUTHORS    Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
TITLE      A combined polymerase chain reaction-colour development
            hybridization assay in a microtitre format for the detection of
            Clostridium spp
JOURNAL    Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
MEDLINE    93356986
PUBMED     7763926
REFERENCE  2 (bases 1 to 138)
AUTHORS    Galindo-Castro,J.F., Rangel,R. and Ramirez,J.L.
TITLE      (no title given)
JOURNAL    Unpublished (1993)
COMMENT    Original source text: Clostridium butyricum (individual isolate Los
            Cortijos) (library: EMBL4-LBB) DNA.
FEATURES   Location/Qualifiers
            source
              1..138
              /organism="Clostridium butyricum"
              /mol_type="unassigned DNA"
              /db_xref="taxon:1492"
              1..138
              /products="16S ribosomal RNA"
              /note="corresponds to position 703 of the E. coli 16S
            rRNA

LOCUS      E05154      137 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Sequence of a DNA fraction prepared by a restriction enzyme HAP II
            from DNA coding for E.coli 16S ribosome RNA.
ACCESSION  E05154
VERSION    E05154.1 GI:2173347
KEYWORDS   JP 1993192147-A/26.
SOURCE     Escherichia coli
ORGANISM   Escherichia coli
REFERENCE  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AUTHORS    Enterobacteriaceae; Escherichia.
TITLE      Shitazu.Y.
JOURNAL    METHOD FOR SPECIFYING DNA BASE SEQUENCE
COMMENT    Patent: JP 1993192147-A 26 03-AUG-1993;
          KIRIN BIBARETSUJI KK
          OS Escherichia coli
          PN JP 1993192147-A/26
          PD 03-AUG-1993
          PF 15-NOV-1991 JP 1991300882
          PI SHIRASU YOSHITARU
          PC C12N15/00,C12Q1/06,C12Q1/68;
          CC strandedness: Doublet;
          CC topology: Linear;
          CC *source: strain-K12.
FEATURES   Location/Qualifiers
            source
              1..137
              /organism="Escherichia coli"
              /mol_type="genomic DNA"
              /db_xref="taxon:562"
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
    |||||
Db 58 GCAACAGGATTAGATACCC 77

RESULT 13
LOCUS      CLORDNA16S      138 bp      DNA      linear      BCT 28-MAR-1994
DEFINITION Clostridium butyricum 16S ribosomal DNA gene.
ACCESSION  L08598
VERSION    L08598.1 GI:144899
KEYWORDS   16S ribosomal DNA.
SOURCE     Clostridium butyricum
ORGANISM   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE  1 (sites)
AUTHORS    Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
TITLE      A combined polymerase chain reaction-colour development
            hybridization assay in a microtitre format for the detection of
            Clostridium spp
JOURNAL    Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
MEDLINE    93356986
PUBMED     7763926
REFERENCE  2 (bases 1 to 138)
AUTHORS    Galindo-Castro,J.F., Rangel,R. and Ramirez,J.L.
TITLE      (no title given)
JOURNAL    Unpublished (1993)
COMMENT    Original source text: Clostridium butyricum (individual isolate Los
            Cortijos) (library: EMBL4-LBB) DNA.
FEATURES   Location/Qualifiers
            source
              1..138
              /organism="Clostridium butyricum"
              /mol_type="unassigned DNA"
              /db_xref="taxon:1492"
              1..138
              /products="16S ribosomal RNA"
              /note="corresponds to position 703 of the E. coli 16S
            rRNA

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ORIGIN      ribosomal DNA gene"
Query Match      100.0%; Score 20; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.8e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
    |||||
Db 77 GCAACAGGATTAGATACCC 96

RESULT 14
LOCUS      LPNEMRRN02      140 bp      rRNA      linear      BCT 23-JUL-1993
DEFINITION F.bozemanae (Legionella) 16S ribosomal RNA.
ACCESSION  M24643
VERSION    M24643.1 GI:175149
KEYWORDS   16S ribosomal RNA; ribosomal RNA small subunit.
SEGMENT    2 of 3
SOURCE     Fluoribacter bozemanae
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Fluoribacter.
REFERENCE  1 (sites)
AUTHORS    Fox,K., Brown,A. and Schnitzer,G.
TITLE      Partial sequence analysis of the 16S-rRNA of Legionellae: Taxonomic
            implications
JOURNAL    Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE  2 (bases 1 to 140)
AUTHORS    Brown,A., Fox,K.F. and Schnitzer,G.
TITLE      Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
JOURNAL    Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT    Original source text: Fluoribacter bozemanae (strain MI-15) rRNA.
FEATURES   Location/Qualifiers
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              /organism="Fluoribacter bozemanae"
              /mol_type="rRNA"
              /strain="MI-15"
              /db_xref="taxon:447"
              <1..>140
              /product="16S ribosomal RNA"
            ORIGIN      About 243 bp after segment 1.
Query Match      100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACAGGATTAGATACCC 20
    |||||
Db 15 GCAACAGGATTAGATACCC 34

RESULT 15
LOCUS      LPNDRTRN02      140 bp      rRNA      linear      BCT 23-JUL-1993
DEFINITION F.dumoffii (Legionella) 16S ribosomal RNA.
ACCESSION  M24642
VERSION    M24642.1 GI:175161
KEYWORDS   16S ribosomal RNA; ribosomal RNA small subunit.
SEGMENT    2 of 3
SOURCE     Fluoribacter dumoffii
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Fluoribacter.
REFERENCE  1 (sites)
AUTHORS    Fox,K., Brown,A. and Schnitzer,G.
TITLE      Partial sequence analysis of the 16S-rRNA of Legionellae: Taxonomic
            implications
JOURNAL    Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE  2 (bases 1 to 140)

```

AUTHORS Brown,A., Fox,K.F. and Schnitzer,G.
 TITLE Tatlockia, a genetically and chemically distinct group of bacteria:
 Proposal to transfer Legionella maceachernii (Brenner, et al.) to
 the genus Tatlockia as Tatlockia maceachernii comb. nov
 JOURNAL Syst. Appl. Microbiol. 14, 52-56 (1991)
 COMMENT Original source text: F.(Legionella) dumoffii (strain Tex-KL)
 ribosomal RNA.

FEATURES
 source Location/Qualifiers
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 /mol_type="rRNA"
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 /note="16S rRNA segment"

ORIGIN About 243 bases after segment 1.

Query Match 100.0%; Score 20; DB 1; Length 140;
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GCAAACAGGATTAGATACCC 20
 |||||
 Db 15 GCAAACAGGATTAGATACCC 34

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 Job time : 877.663 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 164.337 Seconds
(without alignments)
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Title: US-09-940-860-1

Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	23	7	Abv74328 Mycoplasma
2	20	100.0	24	3	Aaa39031 Unknown b
3	20	100.0	37	8	ABX94830 16S rRNA
4	20	100.0	37	8	ABX94859 16S rRNA
5	20	100.0	47	2	AAQ10118 Probe 173
6	20	100.0	50	6	AB159813 Enterococ
7	20	100.0	50	6	AB159817 Peptostre
8	20	100.0	50	6	AB159820 Chlamydia
9	20	100.0	50	6	AB159819 Fusobacte
10	20	100.0	50	6	AB159786 Campyloba
11	20	100.0	50	6	AB159805 Myxococcu
12	20	100.0	50	6	AB159787 Helicobac
13	20	100.0	50	6	AB159796 Salmonell
14	20	100.0	50	6	AB159799 Legionell
15	20	100.0	50	6	AB159801 Caulobact
16	20	100.0	50	6	AB159794 Haemophil
17	20	100.0	50	6	AB159795 Escherich
18	20	100.0	50	6	AB159812 Listeria
19	20	100.0	50	6	AB159816 Clostridi
20	20	100.0	50	6	AB159804 Wolbachia
21	20	100.0	50	6	AB159790 Leptothri
22	20	100.0	50	6	AB159788 Treponema
23	20	100.0	50	6	AB159803 Nitrobact

24	20	100.0	50	6	ABL59792	Ab159792 Neisseria
25	20	100.0	50	6	ABL59791	Ab159791 Thiomicro
26	20	100.0	50	6	ABL59802	Ab159802 Rhodospir
27	20	100.0	50	6	ABL59793	Ab159793 Actinobac
28	20	100.0	50	6	ABL59797	Ab159797 Vibrio Ch
29	20	100.0	50	6	ABL59800	Ab159800 Pseudomon
30	20	100.0	105	6	ABN66212	ABN66212 Streptoco
c 31	20	100.0	122	7	ACD97427	ACD97427 Human col
32	20	100.0	191	7	ABV74330	ABV74330 Mycoplasma
c 33	20	100.0	195	2	AAQ20319	AAQ20319 Region of
c 34	20	100.0	195	4	AAH27463	AAH27463 Polynucle
c 35	20	100.0	279	9	ADC93544	ADC93544 E. faeciu
c 36	20	100.0	279	9	ADC93543	ADC93543 E. faeciu
c 37	20	100.0	312	7	ACD92910	ACD92910 Human col
c 38	20	100.0	312	7	ACD92986	ACD92986 Human col
c 39	20	100.0	312	7	ACD93011	ACD93011 Human col
c 40	20	100.0	312	7	ACD92911	ACD92911 Human col
41	20	100.0	338	7	ACD92089	ACD92089 Human col
42	20	100.0	368	7	ACD92108	ACD92108 Human col
43	20	100.0	442	3	AAC09938	AAC09938 Human sec
44	20	100.0	549	3	AAC95222	AAC95222 Cat flea
45	20	100.0	571	3	AAZ80671	AAZ80671 Human col

ALIGNMENTS

RESULT 1
ABV74328
ID ABV74328 standard; DNA; 23 BP.
XX
AC ABV74328;
XX
DT 29-JAN-2003 (first entry)
XX
DE Mycoplasma 16S rRNA gene PCR primer SEQ ID NO 2.
XX
KW Mollicutes sp; Mycoplasma; 16S rRNA; infection; PCR; primer; ss.
XX
OS Mycoplasma sp.
XX
FN WO200277271-A2.
XX
PD 03-OCT-2002.
XX
PF 25-MAR-2002; 2002WO-DE001154.
XX
PR 25-MAR-2001; 2001DE-01015749.
XX
PA (MINE-) MINERVA BIOLABS GMBH.
XX
PI Vollenbroich D, Schramm C;
XX
DR WPI; 2003-040591/03.
XX
PT Control plasmid, useful as internal standard in amplification method for
detecting Mycoplasma, contains primers that recognize parts of the
Mycoplasma 16S rRNA gene.
XX
PS Claim 2; Page 15; 25pp; German.
XX
CC The invention relates to a control plasmid (A) containing: (a) primers
that recognize a segment of the 16S rRNA-encoding gene in the Mycoplasma
genome; and (b) between the primers an amplicon that includes the
sequence (i). (A) is used as a control in a PCR method for detecting
Mycoplasma in biological materials, e.g. for diagnosing infections or
detecting contamination of cell cultures. (A) provides an internal
control for PCR detection of Mycoplasma to exclude false negatives. The
method is more sensitive and specific than known processes, providing
reliable detection of even very low titers of Mycoplasma and when used in
real-time PCR, has a broad dynamic and linear measurement range, allowing
accurate quantitation. The present sequence is that of a Mycoplasma 16S
rRNA gene PCR primer of the invention

```
XX SQ Sequence 23 BP; 9 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAACAGGATTAGATACCC 20
DB 4 GCAAACAGGATTAGATACCC 23

RESULT 2
AAA39031
ID AAA39031 standard; DNA; 24 BP.
AC AAA39031;
DT 25-AUG-2000 (first entry)
DE Unknown bacterial 16S rRNA gene primer 0776F SEQ ID NO:9.
KW Bacterial; 16S rRNA; identification; polymorphism; microorganism;
KW classification; primer; human medicine; veterinary medicine; agriculture;
KW food science; industrial microbiology; infectious disease; food safety;
KW ss.
OS Unidentified.
XX US6054278-A.
XX 25-APR-2000.
XX 05-MAY-1998; 98US-00073465.
XX 05-MAY-1997; 97US-0045603P.
XX (PEKE ) PERKIN-ELMER CORP.
XX Smith DH, Dodge DE;
XX WPI; 2000-338486/29.
XX Identifying an unknown microorganism by generating a composite sequence
XX of its ribosomal RNA gene region and comparing with composite ribosomal
XX RNA region sequences of distinct microorganisms in a database.
XX Example; Col 10; lipp; English.
XX The present invention describes a method for identifying a microorganism
XX by comparing a composite sequence (I) of a ribosomal RNA gene region with
XX RNA region sequences of unknown microorganisms in a database and
XX identifying the region in the database that matches with (I). (I) is
XX generated by simultaneously obtaining nucleotide base sequence data from
XX every copy of the RNA gene region in the genome of the unknown
XX microorganism. Also described is a method for identifying the species of
XX microorganism by generating (I) and entering it into a first data
XX register of a programmable computer, comparing the first data register
XX with reference data registers that encode a unique composite RNA
XX sequence corresponding to (I) and correlated with unique microorganism
XX species name, and displaying the unique microorganism name correlated
XX with the best matching first data register. The method is useful for
XX identifying microorganisms which are useful in a variety of fields
XX including human medicine, veterinary medicine, agriculture, food science
XX and industrial microbiology. The microorganisms found in patients
XX suffering from an infectious disease can also be identified.
XX Microorganism identification is also useful for monitoring food safety by
XX testing for pathogens. Plants harbouring phytopathogenic bacteria are
XX also identified. The method is convenient and efficient as there is no
XX need to isolate one or more individual 16S rRNA genes. AAA39023 to
XX AAA39039 represent primers for the 16S rRNA gene, which are used in the
XX exemplification of the present invention
```

```
XX SQ Sequence 24 BP; 9 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAACAGGATTAGATACCC 20
DB 2 GCAAACAGGATTAGATACCC 21

RESULT 3
ABX94830
ID ABX94830 standard; DNA; 37 BP.
AC ABX94830;
DT 11-JUL-2003 (first entry)
DE 16S rRNA forward PCR primer SEQ ID 1.
XX Probe; detection; primer; 16S rRNA; amplification; parodontitis; SNP;
XX gene expression pattern; single-nucleotide polymorphism; ss.
XX Unidentified.
XX WO2003014382-A2.
XX 20-FEB-2003.
XX 08-AUG-2002; 2002WO-AT000239.
XX 09-AUG-2001; 2001AT-00001247.
XX (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
XX Mittermayr CR, Ronacher B, Winner F, Zehethofer K;
XX WPI; 2003-256597/25.
XX Device for determining analytes, useful e.g. for detecting bacteria that
XX cause parodontitis, comprises a surface with immobilized analytical and
XX control agents.
XX Disclosure; Page 26; Sipp; German.
XX This invention describes a novel device for detecting analytes in a
XX sample. The device comprises a carrier surface which contains at least
XX one analytical region (including at least one immobilised binding partner
XX for the analyte) and at least one control region which controls of the
XX quality of analysis. The device is particularly used for nucleic acid
XX amplification and detection of (i) bacterial species associated with
XX parodontitis, (ii) gene expression patterns and (iii) single-nucleotide
XX polymorphisms (SNP's). The device provides reproducible, rapid and simple
XX analysis of nucleic acid sequences. The control system is subjected to
XX exactly the same series of operations as the analytical regions, so no
XX extra time for the control step is required and system costs are not
XX significantly more than for analysis without a control. If the device is
XX stored for archiving, the control results are also saved. Many different
XX analytes can be detected simultaneously and controls for many different
XX aspects of analytical quality can be included. This sequence represents
XX an oligonucleotide associated with the detection of 16S rRNA from various
XX bacterial samples, which is used to illustrate the device of the
XX invention
XX Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAACAGGATTAGATACCC 20
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Db 6 GCAACACAGGATTAGATACCC 25

RESULT 4
ABX94859
ID ABX94859 standard; DNA; 37 BP.
XX AC ABX94859;
XX DT 11-JUL-2003 (first entry)
XX DE 16S rRNA detection associated positive control oligonucleotide #3.
XX KW Probe, detection; primer; 16S rRNA; amplification; parodontitis; SNP;
XX OS gene expression pattern; single-nucleotide polymorphism; ss.
XX UNidentified.
XX WO2003014382-A2.
XX PD 20-FEB-2003.
XX PF 08-AUG-2002; 2002WO-AT000239.
XX PR 09-AUG-2001; 2001AT-00001247.
XX PA (LAMB-) LAMEDA LABOR MOLEKULARBIOLOGISCHE.
XX PI Mittermayr CR, Ronacher B, Winner F, Zehethofer K;
XX WPI; 2003-256597/25.
XX PT Device for determining analytes, useful e.g. for detecting bacteria that
PT cause parodontitis, comprises a surface with immobilized analytical and
PT control agents.
XX Claim 22; Page 37; 51pp; German.
XX This invention describes a novel device for detecting analytes in a
CC sample. The device comprises a carrier surface which contains at least
CC one analytical region (including at least one immobilised binding partner
CC for the analyte) and at least one control region which controls of the
CC quality of analysis. The device is particularly used for nucleic acid
CC amplification and detection of (i) bacterial species associated with
CC parodontitis, (ii) gene expression patterns and (iii) single-nucleotide
CC polymorphisms (SNP/s). The device provides reproducible, rapid and simple
CC analysis of nucleic acid sequences. The control system is subjected to
CC exactly the same series of operations as the analytical regions, so no
CC extra time for the control step is required and system costs are not
CC significantly more than for analysis without a control. If the device is
CC stored for archiving, the control results are also saved. Many different
CC analytes can be detected simultaneously and controls for many different
CC aspects of analytical quality can be included. This sequence represents
CC an oligonucleotide associated with the detection of 16S rRNA from various
CC bacterial samples, which is used to illustrate the device of the
CC invention
XX
SQ Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAACACAGGATTAGATACCC 20
Db 6 GCAACACAGGATTAGATACCC 25
RESULT 5
AAQ10118/c
ID AAQ10118 standard; DNA; 47 BP.
XX
XX AAQ10118;
AC

XX 27-AUG-2003 (revised)
DT 09-JAN-2003 (revised)
DT 14-MAR-1991 (first entry)
XX Probe 1739 to the 16S rRNA of Eubacteria.
XX KW ribosomal RNA, ss.
XX OS Eubacteria.
XX WO9015157-A.
XX PD 13-DEC-1990.
XX PF 31-MAY-1989; 89US-00359158.
XX PR 31-MAY-1989; 89US-00359158.
XX PA (GENE-) GENE-TRAK SYST.
XX PI Lane DJ, Buharin A, Weisburg WG;
XX WPI; 1991-007226/01.
XX PT Nucleic acid probes - specific for RNA of Eubacteria, for use in clinical
XX assays.
XX Disclosure; Page 14-16; 58pp; English.
XX Probes allow assay for Eubacteria to be carried out in clinical samples
CC such as blood or urine, in a cost effective and fast manner. The probes
CC require only small sample sizes which may be amplified, with some of the
CC probes suitable as primers. (Updated on 09-JAN-2003 to add missing OS
CC field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 47 BP; 6 A; 15 C; 12 G; 14 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAACACAGGATTAGATACCC 20
Db 33 GCAACACAGGATTAGATACCC 14
RESULT 6
ABL59813
ID ABL59813 standard; DNA; 50 BP.
XX AC ABL59813;
XX DT 18-JUL-2002 (first entry)
XX DE Enterococcus faecalis 16S rDNA fragment #3.
XX KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
XX KW microbial encephalitis; viral encephalitis; ds.
XX OS Enterococcus faecalis.
XX WO200210444-A1.
XX PD 07-FEB-2002.
XX PF 27-JUL-2001; 2001WO-AU000933.
XX PR 28-JUL-2000; 2000AU-00009090.
XX PA (UNSY) UNIV SYDNEY.
XX PI Hunter N, Jacques NA, Martin PE, Nadkarni MA;


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XX WPI; 2002-404428/43.
XX
XX Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
XX Example 12; Fig 1C; 10lpp; English.
XX
XX The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (1) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (1) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (1) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (1) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (1) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
XX Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAACAGGATTAGATACCC 20
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 9
ABL59819
ID ABL59819 standard; DNA; 50 BP.
XX
XX ABL59819;
XX
XX 18-JUL-2002 (first entry)
XX
XX Fusobacterium nucleatum 16S rDNA fragment #3.
XX
XX Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW Microbial encephalitis; viral encephalitis; ds.
XX
XX Fusobacterium nucleatum.
XX
XX WO200210444-A1.
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-AU000933.
XX
XX 28-JUL-2000; 2000AU-00009090.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Hunter N, Jacques NA, Martin FE, Nadkarni MA;
PI

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XX WPI; 2002-404428/43.
XX
XX Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
XX Example 12; Fig 1C; 10lpp; English.
XX
XX The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (1) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (1) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (1) can also be used to
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CC total microbial-derived target material; in assessing encephalitis and
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CC and industrial industries with specific uses including enviroprotection,
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CC control. (1) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
XX Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAACAGGATTAGATACCC 20
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 10
ABL59786
ID ABL59786 standard; DNA; 50 BP.
XX
XX ABL59786;
XX
XX 18-JUL-2002 (first entry)
XX
XX Campylobacter jejuni 16S rDNA fragment #3.
XX
XX Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW Microbial encephalitis; viral encephalitis; ds.
XX
XX Campylobacter jejuni.
XX
XX WO200210444-A1.
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-AU000933.
XX
XX 28-JUL-2000; 2000AU-00009090.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Hunter N, Jacques NA, Martin FE, Nadkarni MA;
PI

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XX DR WPI; 2002-404428/43.
XX
XX PT Polynucleotide useful as primer or probe for determining microbial
XX PT content in sample, has sequence which is comprised by 16S rDNA or 16S
XX PT rRNA, substantially conserved amongst two or more species of
XX PT microorganism.
XX
XX PS Example 12; Fig 1C; 101pp; English.
XX
XX CC The present invention describes a method for determining the total
XX CC microbial content in a sample, comprising amplifying a target nucleotide
XX CC sequence which is substantially conserved amongst 2 or more species of
XX CC microorganisms. Also describes an isolated polynucleotide (I) or its
XX CC complement having a nucleotide sequence which is comprised by 16S rDNA or
XX CC 16S rRNA, substantially conserved amongst two or more species of
XX CC microorganism. (I) can be used: (1) as a primer or probe for determining
XX CC the total microbial content in a sample; (2) as a primer or probe for
XX CC identifying a microorganism by its genus in a sample; and (3) as a probe
XX CC for identifying a particular microorganism or prevalence of a particular
XX CC genus or species of microorganism, in a sample. (I) can also be used to
XX CC identify microorganisms at the genus or species level, and as a trap for
XX CC total microbial-derived target material; in assessing encephalitis and
XX CC distinguishing between microbial and viral encephalitis. (I) is
XX CC applicable to a range of industries including the medical, agricultural
XX CC and industrial industries with specific uses including enviroprotection,
XX CC bioremediation, medical diagnosis, water quality control or food quality
XX CC control. (I) provides an ability to detect bacteria from samples which
XX CC are difficult to cultivate and that would in all practicality remain
XX CC undetected or under-estimated by viable culture count methods and enables
XX CC rapid differentiation of bacteria from viral infections within the
XX CC limited time constraints sometimes experienced in life-threatening
XX CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
XX CC and ABL59822 to ABL59830 represent primers and probes, used in the
XX CC exemplification of the present invention
XX
XX SQ Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. NO. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCACACAGGATTAGATACCC 20
Db 16 GCACACAGGATTAGATACCC 35

RESULT 11
ABL59805
XX AC ABL59805;
XX
XX DT 18-JUL-2002 (first entry)
XX
XX DE Myxococcus xanthus 16S rDNA fragment #3.
XX
XX KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
XX KW microbial encephalitis; viral encephalitis; ds.
XX
XX OS Myxococcus xanthus.
XX
XX PN WO200210444-A1.
XX
XX PD 07-FEB-2002.
XX
XX PF 27-JUL-2001; 2001WO-AU000933.
XX
XX PR 28-JUL-2000; 2000AU-00009090.
XX
XX PA (UNSY ) UNIV SYDNEY.
XX
XX PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

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XX DR WPI; 2002-404428/43.
XX
XX PT Polynucleotide useful as primer or probe for determining microbial
XX PT content in sample, has sequence which is comprised by 16S rDNA or 16S
XX PT rRNA, substantially conserved amongst two or more species of
XX PT microorganism.
XX
XX PS Example 12; Fig 1C; 101pp; English.
XX
XX CC The present invention describes a method for determining the total
XX CC microbial content in a sample, comprising amplifying a target nucleotide
XX CC sequence which is substantially conserved amongst 2 or more species of
XX CC microorganisms. Also describes an isolated polynucleotide (I) or its
XX CC complement having a nucleotide sequence which is comprised by 16S rDNA or
XX CC 16S rRNA, substantially conserved amongst two or more species of
XX CC microorganism. (I) can be used: (1) as a primer or probe for determining
XX CC the total microbial content in a sample; (2) as a primer or probe for
XX CC identifying a microorganism by its genus in a sample; and (3) as a probe
XX CC for identifying a particular microorganism or prevalence of a particular
XX CC genus or species of microorganism, in a sample. (I) can also be used to
XX CC identify microorganisms at the genus or species level, and as a trap for
XX CC total microbial-derived target material; in assessing encephalitis and
XX CC distinguishing between microbial and viral encephalitis. (I) is
XX CC applicable to a range of industries including the medical, agricultural
XX CC and industrial industries with specific uses including enviroprotection,
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XX CC are difficult to cultivate and that would in all practicality remain
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XX CC rapid differentiation of bacteria from viral infections within the
XX CC limited time constraints sometimes experienced in life-threatening
XX CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
XX CC and ABL59822 to ABL59830 represent primers and probes, used in the
XX CC exemplification of the present invention
XX
XX SQ Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. NO. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCACACAGGATTAGATACCC 20
Db 16 GCACACAGGATTAGATACCC 35

RESULT 12
ABL59787
XX AC ABL59787;
XX
XX DT 18-JUL-2002 (first entry)
XX
XX DE Helicobacter pylori 16S rDNA fragment #3.
XX
XX KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
XX KW microbial encephalitis; viral encephalitis; ds.
XX
XX OS Helicobacter pylori.
XX
XX PN WO200210444-A1.
XX
XX PD 07-FEB-2002.
XX
XX PF 27-JUL-2001; 2001WO-AU000933.
XX
XX PR 28-JUL-2000; 2000AU-00009090.
XX
XX PA (UNSY ) UNIV SYDNEY.
XX
XX PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

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XX WPI; 2002-404428/43.
 XX
 XX Polynucleotide useful as primer or probe for determining microbial
 PT content in sample, has sequence which is comprised by 16S rDNA or 16S
 PT rRNA, substantially conserved amongst two or more species of
 PT microorganism.
 XX
 XX Example 12; Fig 1C; 10lpp; English.
 XX
 XX The present invention describes a method for determining the total
 CC microbial content in a sample, comprising amplifying a target nucleotide
 CC sequence which is substantially conserved amongst 2 or more species of
 CC microorganisms. Also describes is an isolated polynucleotide (1) or its
 CC complement having a nucleotide sequence which is comprised by 16S rDNA or
 CC 16S rRNA, substantially conserved amongst two or more species of
 CC microorganism. (1) can be used: (1) as a primer or probe for determining
 CC the total microbial content in a sample; (2) as a primer or probe for
 CC identifying a microorganism by its genus in a sample; and (3) as a probe
 CC for identifying a particular microorganism or prevalence of a particular
 CC genus or species of microorganism, in a sample. (1) can also be used to
 CC identify microbial-derived target material; in assessing encephalitis and
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 CC are difficult to cultivate and that would in all practicality remain
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 CC limited time constraints sometimes experienced in life-threatening
 CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
 CC and ABL59822 to ABL59830 represent primers and probes, used in the
 CC exemplification of the present invention
 XX
 XX Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAACAGGATTAGATACCC 20
 Db 16 GCAACAGGATTAGATACCC 35
 RESULT 13
 ABL59796
 ID ABL59796 standard; DNA; 50 BP.
 XX
 XX ABL59796;
 XX
 XX 18-JUL-2002 (first entry)
 DT
 XX
 XX Salmonella typhi 16S rDNA fragment #3.
 DE
 XX
 XX Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
 KW microbial encephalitis; viral encephalitis; ds.
 XX
 XX Salmonella typhi.
 OS
 XX WO200210444-A1.
 PN
 XX 07-FEB-2002.
 PD
 XX
 XX 27-JUL-2001; 2001WO-AU0000933.
 PF
 XX 28-JUL-2000; 2000AU-00009090.
 PR
 XX (UNSY) UNIV SYDNEY.
 XX
 XX Hunter N, Jacques NA, Martin FE, Nadkarni MA;
 XX
 PI

XX WPI; 2002-404428/43.
 XX
 XX Polynucleotide useful as primer or probe for determining microbial
 PT content in sample, has sequence which is comprised by 16S rDNA or 16S
 PT rRNA, substantially conserved amongst two or more species of
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 XX
 XX Example 12; Fig 1C; 10lpp; English.
 XX
 XX The present invention describes a method for determining the total
 CC microbial content in a sample, comprising amplifying a target nucleotide
 CC sequence which is substantially conserved amongst 2 or more species of
 CC microorganisms. Also describes is an isolated polynucleotide (1) or its
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 CC microorganism. (1) can be used: (1) as a primer or probe for determining
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 CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
 CC and ABL59822 to ABL59830 represent primers and probes, used in the
 CC exemplification of the present invention
 XX
 XX Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAACAGGATTAGATACCC 20
 Db 16 GCAACAGGATTAGATACCC 35
 RESULT 14
 ABL59799
 ID ABL59799 standard; DNA; 50 BP.
 XX
 XX ABL59799;
 XX
 XX 18-JUL-2002 (first entry)
 DT
 XX
 XX Legionella pneumophila 16S rDNA fragment #3.
 DE
 XX
 XX Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
 KW microbial encephalitis; viral encephalitis; ds.
 XX
 XX Legionella pneumophila.
 OS
 XX WO200210444-A1.
 PN
 XX 07-FEB-2002.
 PD
 XX
 XX 27-JUL-2001; 2001WO-AU0000933.
 PF
 XX 28-JUL-2000; 2000AU-00009090.
 PR
 XX (UNSY) UNIV SYDNEY.
 XX
 XX Hunter N, Jacques NA, Martin FE, Nadkarni MA;
 XX
 PI

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CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
XX Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
Db |||||
16 GCAACACAGGATTAGATACCC 35

RESULT 15
ABL59801
AC ABL59801 standard; DNA; 50 BP.
XX
XX ABL59801;
XX
XX 18-JUL-2002 (first entry)
XX
XX Caulobacter vibrioides 16S rDNA fragment #3.
DE
XX
XX Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
XX Caulobacter vibrioides.
OS
XX
XX WO200210444-A1.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 27-JUL-2001; 2001WO-AU000933.
PF
XX
XX 28-JUL-2000; 2000AU-00009090.
PR
XX
XX (UNSY ) UNIV SYDNEY.
PA
XX
XX Hunter N, Jacques NA, Martin PE, Nadkarni MA;
PI

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XX WPI; 2002-404428/43.
XX
XX Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
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XX
XX Example 12; Fig 1C; 101pp; English.
XX
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CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (1) or its
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CC 16S rRNA, substantially conserved amongst two or more species of
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CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (1) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
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CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (1) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
XX Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACACAGGATTAGATACCC 20
Db |||||
16 GCAACACAGGATTAGATACCC 35

Search completed: August 4, 2004, 06:43:33
Job time : 166.337 secs

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